

# STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 133468

TO: Phuong Bui

Location: REM/2A15/2C18

Art Unit: 1638

Monday, September 27, 2004

Case Serial Number: 10/624061

From: Deirdre Arnold

**Location: Biotech-Chem Library** 

**REM 1A64** 

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

#### Search Notes

### **RUSH**

Results are for SN 10/624,061.

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,

Deirdre Arnold



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10:

Q987h4 arabidopsis Q98tb2 lycopersico Q98tb2 lycopersico Q9340 oryza sativ Q0544 arabidopsis Q95460 arabidopsis Q95408 pichia angu Q99td8 pichia angu Q9581 prunis aviu Q22410 petroselinu Q22409 petroselinu Q22409 petroselinu Q9147 plasmodium Q9405 Q97sj4 streptococc Q8puq5 methanosarc Q8egx5 shewanella Q9S7H4 Q9STB2 Q9STB2 Q9C544 Q9KF60 Q9FAD8 Q9PAD8 Q9 Q97SJ4 Q8PUQ5 Q8EGX5 29AHC6 1000 16 17 333 Query Match Length DB 4057 448.9 32.3 30.9 24.6 121.1 14.0 6685.5 6669.5 6669.5 6432 4432 4423 2283 2283 110 110 107 107 108 108 108 109 109 109 Score

Result No.

**BLOSUM62** 

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Title: Perfect score:

Seguence:

OM protein

Run on:

SEQUENCE FROM N.A.

Kuhn R., Vogt E., Schmid J., Amrhein N., Schaller A.;

"Expression analysis of Arabidopsis thaliana genes for plastidic (CM1)
and cytosolic (CM2) chorismate mutases.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. [2]
SEQUENCE FROM N.A.
MEDLINE=9111372; PubMed=8953244;
Eberhard J., Ehrler T.T., Epple P., Felix G., Raesecke H.R.,
Amrhein N., Schmid J.;
"Cytosolic and plastidic chorismate mutase isozymes from Arabidopsis
"Cytosolic and plastidic chorismate mutase isozymatic properties."; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chorismate mutase (EC 5.4.99.5) (Putative chorismate mutase CM2).
CM2 OR T30N20 140 OR AF3010870.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids; II; Brassicales; Brassicaceae, Arabidopsis. thaliana: molecular characterization and enzymatic properties."; Plant J. 10:815-821 (1996). 3 SEQUENCE FROM N.A. Bevan M., Dirkse W., Stiekema Bancroft I., Mewes H.W., Rudd S., Lemcke X., Mayer K.F.X.; Submitted (JUL-2000) to the EMBL/GenBark/DDBJ databases. EU Arabidopsis sequencing project; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases SEQUENCE FROM N.A. SEQUENCE FROM N.A DDTTDDDTTDDDTTDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDTTDDDTTTDDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDTTTDDTTDDDTTTDDTTDDDTTTDDTTDDTTDDDTTTDDTTDDDTTTDDTTDDDTTTDDTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDDTTTDDTTDTTDDTTTDDTTDTTDDTTDTTDDTTDTTDDT

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
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Last annotation update)
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51.6%; Score 691; DB 10;
Best Local Similarity 55.7%; Pred. No. 1.1e-49;
Matches 137; Conservative 39; Mismatches 68;
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                    Solanales; Solanaceae; Solanum
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MEDLINE=96400046; PubMed=8806422;
                                                                                                                                                          chorismate mutase.";
Plant Mol. Biol. 31:917-922(1996)
EMBL; L47156; AAD48923.1; -.
HSSP; P32178; 2CSM.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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P0403C05.9.
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                                                                           SEQUENCE FROM N.A.
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                      lamiids; Solanale
NCBI_TaxID=4081;
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Yamada K., Chan N.A., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W.,

Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C.,

Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C.,

Wu H.C., Yu G., Yuan S., Bowser L., Carninci P., Chen H., Cheuk R.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M.,

Palm C.J., Sakurai T., Saton M., Seki M., Shinn P., Southwick A.,

Palm C.J., Sakurai T., Saton M., Seki M., Shinn P., Southwick A.,

Rhinozaki K., Davis R.W., Ecker J.R., Theologis A.,

Shinozaki R., Davis R.W., Ecker J.R.,

Shinozaki R., Davis R.W., Ecker J.R.,

Shinozaki R., Davis R.W., Ecker J.R.,

Shinozaki R., Satonerase activity, IEA.

GO, GO:0010683; F:dorerase activity, IEA.

GO, GO:0010683; P:aromatic amino acid family biosynthesis, IEA.
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Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriuni M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carminci P., Chen H., Cheuk R., Hayashizani Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Linh J., Meyers M.C., Mirzanda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A., "Full Length, Char & A5510870 (GI:15238285).", Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chorimate mutase (EC 5.4.95).
Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Best Local Similarity 61.1%; Pred. No. 2.7e-60;
Matches 162; Conservative 31; Mismatches 68;
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PIRSF; PIRSF017318; Chor_mut_AroQ_eu; 1.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                  GO, GO:0004106; F:chorismate mutase activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
INTERPO: IPR002701; Chorismate mut II.
InterPro: IPR008281; Chorismat mut II.
InterPro: IPR00838; Chorismat mut II.
Ffam; PF01817; Chorismate mut; 1.
PRAS: PIRSF017318; Chor_mut_AroQ-eu.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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Q9XF60
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MEDLINE=21016719; PubMed=11130712;

MIDLINE=21016719; PubMed=11130712;

Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fuji C.Y.,

dill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-B.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Neoney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Verter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                    SLVEFWYRETEKLHQQVGRYKSPDEHPFFPBDLPEPLLYPLQYPKVLHPIADSININKEI 152
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01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Chorismate mutase, putative (Putative chorismate mutase, 16810-15349)
(AL1969370).
F10113.6 OR F33010.5 OR AT1G69370/F23010_5.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                      1,
    P:aromatic amino acid family biosynthesis; IEA
                                                                                                            DB 10; Length 294;
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51.2%; Score 685.5; DB 10
51.5%; Pred. No. 3.7e-49;
ive 45; Mismatches 81;
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                           Query Match
Best Local Similarity 51.5
Matches 135, Conservative
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SEQUENCE FROM N.A.
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Q9C544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 DESEYLKLESIRHSLIRQEDSIIFNLLERAQYRYNADTYDEDAFTWEGFQGSLVBFWVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 MKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDND-NENRKFDPSVASSLYKNWVIPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 TEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL
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                   K., Ishida J.,
rominci P., Kawai J.,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                          Chan M.M., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishinda J., Jones T., Kamiya A., Karlin.Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO13364; AAG54971; -

EMBL, AK117860; BAC425011; -

EMBL, AK117860; BAC425011; -

EMBL, BT003305; AAG633701; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P32178; 2CSM.

GO; GO:0004106; F:chorismate mutase activity; IEA.

GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.

InterPro; IPR003701; Chorismate_mut.

InterPro; IPR008951; Chorismate_mut II.

InterPro; IPR008238; Chor mut AroQ eu.

Pfam; PF01817; Chorismate_mut AroQ eu.

PRSF; PIRSF017318; Chor mut AroQ eu.

PRSF; DIRSF017318; Chor mut AroQ eu.

PRSF; DIRSF017318; Chor mut AroQ eu.

PRSF; DIRSF017318; Chor mut AroQ eu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Length 316;
STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida .
Sakajima M., Enju A., Kaniya A., Narusaka M., Carninci P., F
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.0%; Score 669.5; DB 10; Length Best Local Similarity 51.4%; Pred. No. 8.8e-48; Matches 130; Conservative 44; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Mobley E., Kunkel B., Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 KEVQIEYLLRRLD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 KEVQVEYLLRRLD 261
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                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                 ATSGD-DGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20353451; PubMed=10894726;

Krappmann S., Pries R., Gellissen G., Hiller M., Braus G.H.;

Krappmann S., Pries R., Gellissen G. Hiller M., Braus G.H.;

"HARO7 encodes chorismate mutase of the methylotrophic yeast Hansenula

polymorpha and is derepressed upon methanol utilization.";

J. Bacteriol. 182:4188-4197(2000).

EMBL, ARPO4738; AAF87954-1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 LITFISVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLYKNWVIPLIKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTEALQAKAGRYKNPEENAFFP-ENLPPSIVPSYSFKQFLHPGAA---SININKSIWKMY
                              128 VEHIVPGITGAGKGKTESEDDGNYGSSATRDVEVLQALSRRIHFGMFVSESKFLAAPHNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 VLDLGNIRDALVRMEDTIIFNFIERSQFYASPSVYKVNQFPIPNFDGSFLDWLLSQHERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 QAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELLP-LL
                                                                            DDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKNTEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004106; F:chorismate mutase activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0009073; P:isomerase activity; IEA.
InterPro; IPRO02701; Chorismate mut.
InterPro; IPRO08951; Chorismate mut.
InterPro; IPRO08238; Chor mut. AroO_eu.
PFGM; PF01817; Chorismate_mut: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%; Score 423; DB 3; Length 280; 38.0%; Pred. No. 3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AA; 32068 MW; 689D49312CD292D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Chorismate mutase (EC 5.4.99.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
                                                                                                                                                                                                            49; Mismatches
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95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q9P4D8;
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                                                                                                                                                                                                                                                                                  10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes;
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogen Cryptococcus neoformans.")
Submitted (UTM-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (UTM-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AF394889; AAR83369.1;
GO; GO:0004106; F:AhOrismate mutase activity; IEA.

GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
InterPro; IPR002701; Chorismate mut II.
InterPro; IPR008238; Chorismate mut II.
InterPro; IPR008238; Chorismate continuity
Pfam; PF01817; Chorismate mut I.
BIRSF; PF01817; Chorismate mut I.
SEQUENCE 295 AA; 33294 MW; EIÄ74EI85DFC855A CRC64;
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                                                              GO, GO:0004106; F:chorismate mutase activity; IEA.
GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
InterPro; IPR002701; Chorismate_mut.
InterPro; IPR008238; Chorismate_mut_II.
InterPro; IPR008238; Chor_mut_ĀroQ_eu.
Pfam; PF01817; Chorismate_mut_I.
PIRSF; PENSF017318; Chor_mut_AroQ eu; 1.
SEQUENCE 316 AA; 36621 MW; P4B654A9CD065ABB CRC64;
                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                   DB 10; Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.3%; Score 432; DB 3; Length 295; Best Local Similarity 36.8%; Pred. No. 5.6e-28; Matches 100; Conservative 56; Mismatches 96; Indels 3
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"Identification of five amino acid biosynthesis genes from
                                                                                                                                                                                                                 48.9%; Score 654.5; DB 10; Length 50.6%; Pred. No. 1.6e-46; ive 44; Mismatches 80; Indels
"CM-3, a novel Arabidopsis gene encoding chorismate muta
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131219; AAD21624.1; -.
HSSP; F32178; 2CSM.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVQVEYLLRRLD 261
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                                                                                                                                                                                                                                                    Matches 128; Conservative
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                                                                                                                                                                                                                                    Similarity
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132

Q9Y7B2

RESULT 8

OGYAPA

OGYA

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76 KAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKNYFKELLPLLATS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petroselinum crispum (Parsley) (Petroselinum hortense).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
campanulids; Apiales; Apiaceae; Apioideae; apioid superclade;
Apium clade; Petroselinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKLLTF
Juna, youd; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eddicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
NCBI_TaxID=42229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Balbrock K.; Logemann E., Reinold S., Hahlbrock K.; Logemann E., Reinold S., Hahlbrock K.; Logemann et allottor "Extensive reprogramming of cellular metabolism by fungal elicitor infection in parsley suggests a new perception of 'defense-related'
                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004106; F:chorismate mutase activity; IEA.
GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
InterPro; IPR002701; Chorismate mut.
InterPro; IPR008951; Chorismat_mut_II.
Pfam; PF01817; Chorismate_mut; 1.
NON TER.
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EMBL; AF012867; AAB69323.1; -
EMBL; AF012867; AAB69323.1; -
EIR; T14902, T14902.
HSSP; P31178; 5CSM.
GO; GO:0004106; F:chorismate mutase activity; IEA.
GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
InterPro; IPR008201; Chorismate mut.
InterPro; IPR008951; Chorismat mut.II.
PF01817; Chorismate_mut.II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 131;
                                                                                                                                                                                                                                                                             Kitts H.B.;
Thesis (1998), Department of Biology, Imperial College of Technology & Medicine, London, U.K.
EMBL; AJ004916; CA406216.1; -.
HSSP, P32178; 5CSM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                                                                                                Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 131 131 131 131 131 AA; 14808 MW; 8C7F65F7FBCB1A03 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 329; DB 10;
48.8%; Pred. No. 7.8e-20;
iive 23; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AA
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01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                       Bing;
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NCBI_TaxID=4043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 TSV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 PTV 126
                                                                                                                                                       STRAIN=cv. Bin
Coutts R.H.A.;
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01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 PAICPQFGGREDRGETQENYGSAATCDVSCLQALSRRIHFGKFVAESKFQKETEKFVALI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 RAKDKEGLMKLLIFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLYK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 DASKALDLANIRFQLIRLEDTITFHLIBRVQFPLNKTIYIPGGVKIPNEQISLMDYLLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-9935771; pubMed=10428795;
Krappmann S., Helmstaadt K., Gerstberger T., Eckert S., Hoffmann B., Hopppert M., Schnappauf G., Braus G.H.;
Hopppert M., Schnappauf G., Braus G.H.;
"The aroC gene of Aspergilus nidulans codes for a monofunctional, allosterically regulated chorismate mutase.";
J. Biol. Chem. 274:22275-22282(1999).
HSSP: P313741; AAD30065.1; -.
HSSP: P32178; 2CSM.
GO: 0004166; F: chorismate mutase activity; IEA.
GO: GO: 00016853; F: isomerase activity; IEA.
GO: GO: 0009073; P: aromatic amino acid family biosynthesis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                  Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.9%; Score 414; DB 3; Length 267; 35.5%; Pred. No. 1.6e-26; Live 54; Mismatches 99; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 AA; 30661 MW; 72FB25CAB2291593 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chorismate mutase (EC 5.4.99.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AA.
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PIRSF; PIRSF017318; Chor_mut_AroQ_eu; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002701; Chorismate mut.
InterPro; IPR008951; Chorismat_mut_II.
InterPro; IPR008238; Chor_mut_AroQ_eu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 EYVIPLTKVVEVEYLMQRL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-A00-1998 (TrEMBLrel. 07, CA
01-NOV-1998 (TrEMBLrel. 08, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Chorismate mutase (Pragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.5
nes 92; Conservative
                                                                                                                                                     PRELIMINARY;
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                                               256
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EVDYLLRRLE
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Streptococcus pneumoniae.
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01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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1834 FL 1835
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Q9AHC6
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                                                                                                                                                             88 FFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQTAAN 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petroselinum crispum (Parsley) (Petroselinum hortense).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolitophyta; eudicotyledons; core eudicots; asterids;
campanulids; Apiaceae; Apiaceae; Apioideae; apioid superclade;
Apium clade; Petroselinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PEHL.PEPIS.PLQYPQVIAPVTESININSKIWDMYFRNLVERLVKEGEDGNYGATAVCDT
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"Extensive reprogramming of cellular metabolism by fungal elicitor
infection in parsley suggests a new perception of 'defense-related'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
PRIO 0251.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188; DB 10; Length 70;
Pred. No. 2e-08;
8; Mismatches 26; Indels
                                                                           Length 82;
                                                                                                                       Indels
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EMBL, AF012866; AAB69322.2; -.
PIR, T14901, T14901.
EMSPP, P32178; 5CSM.
InterPro; IPR008951; Chorismat_mut_II.
  1 1
82 82
82 AA; 9154 MW; AF5A191C43D5030B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 AA; 7917 MW; 5D2D266E7ACA3843 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                       20;
                                                                             Score 283; DB 10;
Pred. No. 2.9e-16;
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                                                                                21.1%; Score 283; DB 63.4%; Pred. No. 2.9e
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                                                                                                                                                                                                                                                                                                                                                                                        70
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                                                                                                                                                                                                                                           148 DLSLLQSISRRIHYGKFVAEVK 169
                                                                                                                                                                                                                                                                                  61 DLOCLOAISRIHYGKFVABAK 82
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1 Similarity 51.4%;
36; Conservative
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                                                                                                                           52; Conservative
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                                                                                Query Match
Best Local Similarity
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MEDIINE=2255705; PubMed=12368664;

Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

Carlton J.M., Paln A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S.,

Pertea M., Allen J., Salengut J., Hafter M., Waldya A.B.,

Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,

Wonter J.C., Cartoci D.J., Hoffman S.L., Newbold C., Davis R.W.,

Fraser C.M., Barrell B.,

"Genome sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 VKNTEAIQAKA-GRYKNPE-----ENAFFPENLPPSIVPSYSF---KQFLHPGAASINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1612 IKKIQTYYINTLQKYKNNBIKKCTNDSEYF-----SELINTYKYHCEFFFIYP-----QI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 -----LLQSISRRIHYGKFVAEVKFRDAPQ-DYEPLIRAKDKEGLMKLLIFTSVEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VYTLASVREDLVRQEDĮIIYGLIERAKFPSŅ----SHTYDEKY---AQIQGFCGSLVBFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Indels 84; Gaps
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MEDLINE-INVO.
MEDLINE-INVO.
MEDLINE-INVO.
Medlecular characterization of Streptococcus pneumoniae tynand lac capsular polyaaccharide gene clusters.";
and lac capsular polyaaccharide gene clusters.";
Immin. 6:1244-1255(2001).
EMBI, AF316639, AAK20675-1;
GO: GO:0005622, C:intracellular; IEA.
GO: GO:0005840, C:ribosome; IEA.
GO: GO:000168; F:methyltransferase activity; IEA.
GO: GO:000168; F:methyltransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | "Gencom.";
| Talling arm.";
| Nature 419:498-511(2002).
| Nature 419:498-511(2002).
| Embl., AE014833; AAN35448.1; -.
| Hypothetical protein.
| Hypo
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 8.2%; Score 110; DB Local Similarity 21.2%; Pred. No. 15; es 64; Conservative 63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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NCBI_TaxID=2209;
SEQUENCE
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Q8PUQ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 EENAFFPENLPPSIVPSYSFKOFLHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQ 143
                                                                                                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIYGLIERAKFPSNSHT----YDEKYAQIQGFCGSLVEFVVKNTEAIQAKAGRYKNP
                                                                                                                                                                                                                                                                                                                                       58;
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GO; GO: 0005640; C:ribosome; IEA.
GO; GO: 0005840; C:ribosome; IEA.
GO; GO: 00058168; F:metryltransferase activity; IEA.
GO; GO: 0003135; F:structural constituent of ribosome; IEA.
GO; GO: 0008152; P:metabolism; IEA.
GO; GO: 0008152; P:metabolism; IEA.
InterPro; IPR001345; P:protein biosynthesis; IEA.
InterPro; IPR001345; PS pyruv trans.
InterPro; IPR001865; Ribosomal S2.
PFam, PP04210; PS pyruv trans.
IPROSITE; PS00962; RIBOSOMAL S2.; I.
Hypothetical protein; Complète proteome.
                                                                                                                                                                                                                                                                             DB 2; Length 355;
                                                                                                                                                                                                                                                                          8.0%; Score 107; DB 2; Length 35:
23.8%; Pred. No. 1;
tive 36; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 KLLIFISVEETVRKRV-----EKKAV-VFGOEVNLNSDDNDN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                   GO; 0006412; P:protein biosynthesis; IEA.
InterPro; IPR000878; Cor/por_Meransf.
InterPro; IPR001865; Ribosomal_S2.
Pfam; PF04230; PS_PYRV trans.
PROSTIE; PS050962; RIBOSOMAL S2 1; 1.
SEQUENCE 355 AA; 40777 MW; 608DC233A233D6E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein SP0355.
                            protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
      GO:0008152; P:metabolism; IEA GO:0006412; P:protein biosyntl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecience 293;498-506(2001).
EMBL; AE007347; AAK74528.1; -.
PIR; G95041; G95041
                                                                                                                                                                                                                                       Query Match
Query Local Similarity 20..
Best Local Similarity 20..
Than 53; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae.
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NCBL TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
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1097834
10097834
10097834
1001-0C
DT 011-0C
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Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Bacumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
Fritz H.-J., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                 31 IIYGLIERAKF-----PSN-SHTYDEKYAQIQGFCGSLVEFVVKNTEAIQAKAGRYKNP
                                                                                                                                                                                                                              26 IVYDLLESKGYEVSFYNPSDFFQMYLKEYRQKQ-----SFTKKQADALLYIPGGYFGE
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R InterPro; IPR003594; His kinase.

R InterPro; IPR001540; His kinase.

R InterPro; IPR001610; PAS-assoc C.

R InterPro; IPR0010014; PAS-domain.

R Pfam; PF007818; PAS; 1.

R TIGRAMA; TIGRO0229; Sensory_box; 6.

R PROSITE; PS50113; PAC; 5.

R PROSITE; PS50113; PAC; 5.

R RP0031E; PS50113; PAC; 5.

R RP0031E; PS50113; PAC; 5.

R RP0031E; PS50113; PAC; 5.

R RF0031E; PS50113; PAC; 6.

R RF0031E; PS50113; PAC; 7.

R RF0031E; PS50113; PAC; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome of Methanosarchina mazei: evidence for lateral gene transfer between Bacteria and Archaea.";
"Mol. Microbiol. Biotechnol. 4:453-461(2002).

EMBL; AE013469; ABJ3073.1;
GO; GO:001651; F:ATP binding; IEA.

GO; GO:001670; F:kinase activity; IEA.

GO; GO:00155; F:two-component sensor molecule activity; IEA.

GO; GO:000160; F:two-component signal transduction system (p.
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                                                                                                                     58;
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                                                      7.8%; Score 105; DB 16; Length 360; 24.7%; Pred. No. 1.6; tive 34; Mismatches 76; Indels 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sedis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | : : | : : | | | | 175 EQLCQLKREAKDKKIILVHYNHSKKALEKFAESISLFLENNFN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanosarcina mazei (Methanosarcina frisia).
Archaea, Buryarchaeota, Euryarchaeota orders incertae
Methanosarcinales, Methanosarcinaceae, Methanosarcina.
360 AA; 41405 MW; EC03E7E13AC357F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-GOel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein MM2277 (EC 2.7.3.-).
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                                         Query Match
Best Local Similarity 24.7%
".rhes 55; Conservative
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Best Local Similarity 25.9
Matches 59; Conservative
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9 PDSGNVYILASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGS 61	298 PDD-REYLINSIKKDFDEQIRNIDYRIVLPPGEERTVRTRVEITFDEENQPVRAEGIVQD 356	62 LVEFVVKNTE-AIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSI 120	357 ITELKRIEKALQEREEQYRAFF-ENSMDAVLFASPDGTIHAANKAA 401	121 WKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDA 173	402 CKTFGMTEKEIIRAGRNGIVDQSDPRLKPSLEERNSTGRFKGEINHKRKDGTI 454	174 -PQDYEPLIRAKDKEGLMKLLTFTSVEETVRKRVEKKAVVF 213	455 FPGEVSTAL-FXDKNGLMXIVIIIRDITERKKAREEVLRKSBEHYRMLF 501
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Search completed: September 25, 2004, 02:54:17 Job time: 72 secs

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GenCore version 5.1.6
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OM nucleic - nucleic	ic search, using sw model
	ember 24, 2004, 22
Title: US-10 Perfect score: 1020 Sequence: 1 gc	US-10-624-061-15 1020 1 gcacgagagcttaàtttcaaatcttcaaaaaaaaaaa 1020
Scoring table: IDE Gap	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 347	3470272 seqs, 21671516995 residues
Total number of hits	ts satisfying chosen parameters: 6940544
Minimum DB seq leng Maximum DB seq leng	ength: 0 ength: 2000000000
Post-processing: Mi Ma Li	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : 1. General description	GGENEMD1:*  (GPD Da:*  (GD

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ž.,	AK404683 Sequence	stabilence semience	ARSJOOJ SEGICE	AX343933 Sequence	AX464575 Sequence	AX464581 Sequence	L47355 Arabidopsis	rabiĝop	equence	AX343935 Sequence	L47356 Lycopersico	ednence	AK068983 Oryza sat	rabidop	AR236633 Sequence	AR236639 Sequence	AX464574 Sequence	AX464580 Sequence	Z26519 A.thaliana	AX506042 Sequence	AR404686 Sequence	AKIUIZZO Oryza sat	DECOMPOSE DECICE	AKO69725 Orvza sat	AK105512 Oryza sat	AK117860 Arabidops	BT005306 Arabidops	AR236635 Sequence	AR236641 Sequence	AX464576 Sequence	ednence	AF131219 Arabidops	AR404684 Sequence	ACLZ8660 Medicago	בשפח דושות	thorac a	249219 S. Cerevisia	in the variation	ucleic	equence				•	1:000 10-01 TAG 7:0003	- 1110ar - 121-120								
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OY 961 TTTCATCGGCTTTATTAGGAAAGGCATTATTATATCATGATCTTCAAAAAAAA	RESULT 2 AR404683 LOCUS DETAILTION Sequence 5 from patent US 6627798. ACCESSION AR404683. VERSION VERSION AR404683. AR40483. AR404683. AR40483. AR40483. AR40483. AR40483. AR40483. AR404683. AR40483. AR404683. AR40483.	Query Match Best Local Similarity 95.4%; Score 465.6; DB 6; Length 525; Best Local Similarity 95.4%; Pred. No. 1.5e-98; Matches 499; Conservative 0; Mismatches 22; Indels 2; Gaps 2;  Qy 8 AGCTTAATTTCAAGAATGGCCAAAGCAGCACAAAGTATTCTGGGAATGTGTAC 67	68 61 128	121 ATTGAGAGAGCCAAGTTCCCTAGCAATTCTCACACCTATGAAAAGTATGCTCAAATC 1 188 CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTGTTAAGAATACAGAGCCATTCAAGCT 2 181 CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCATTCAAGCT 2 181 CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCATTCAAGGT 2	QY         248 AAGGCTGGAAGATACAAAACCCTGAAGAAAACGCTTCTTCCCAGAAATTTACCACCA 307           11		ř	RESULT 3 AV133840 LOCUS LOCUS LOCUS DEFINITION Arabidopsis thaliana clone U18739 putative chorismate mutase CM2 (At5g10870) mRNA, complete cds. ACCESSION AY133840.1 GI:22136859
source 1. 1020 /organism="unknown" /mol_type="genomic DNA"	Query Match         100.0%;         Score 1020;         DB 6;         Length 1020;           Best Local Similarity 100.0%;         Pred. No. 1.7e-228;         0;         Indels 0;         Gaps 0;           Matches 1020;         Conservative 0;         Mismatches 0;         Indels 0;         Gaps 0;           QY         I GCACGAGAGCTTAATTTCAAGAATGGCCAAAGCAGAACAAAGTCCTGATTCTGGGAA 60         0         0           Db         I GCACGAGAGCTTAATTTCAAGAATGGCCAAAGCAGAACAAAGTCCTGATTCTGGGAA 60         0           QY         61 TGTGTACACGCTAAGCTTCTGTGAGAGGAATTGGTTAGGCAAAGTCCTGATTTA 120           Db         61 TGTGTACACGCTAAGCTTCTGAGAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTA 120           QY         121 TGGTCTCATTGAGAGAGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAATTGT 180           Db         121 TGGTCTCATTGAGAGAGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAATTGTGT         180           Db         181 TCAAATCCAGGATTTTTGTGGTAATTGTTGTTAAGAATACAAGAGCCAT 240           Db         181 TCAAATCCAGGGTTTTTGTGGTGAATTTGTTGTTAAAAAAAA			421 TACTICGGGTGAIGGCAACTAIGCGCAAACIGCAGGCTAAIGACTITICAITAITGCA 481 GTCCAICTCTAGAAGAITCACTAIGGGAAAGTITGIAGGGGGGGGGG	QY         541         TCCTCAAGACTACGAGCCTTTAATTCGAGCTAAGGATAAAGATGATTGTT         600           bb         541         TCCTCAAGACTACGAGCTTAATTCGAGCTAAGGATAGAGAGAATTGTGAAATTTGTT         600           cor         601         GACATTTACAAGCGTTGAAGAAGAGAGAGAGAGAGAGAGA	TGGGCAGGAAGTGAATCTTAACAGTGATGACAATGACAATGAAAACCGTAAATTTGATCC	Db 721 ATCAGTGGCTTCTACCTTGTACAAAATTGGGTGATACCTCTCACCAAGGAGGTTCAGGT 780 Qy 781 TGAGTACCTCTTGCGCCGTCTAAACGATTACAATGCAGTTAGAATTTAGAAGAA 840 Db 781 TGAGTACCTCTTGCGCCGTCTAGAAGCATTACAATGCAGTTAGAATTTAGAAGAA 840	QY         841         TGGAAGATGAATATGATGTTGTTCAAATGATTAAGCTCTTAAGTGATCCTTTATTGC         900           DD         841         TGGAAGATGAATGATGTTGTTGTTCAAATGATTAAGCTCTTAAGTGATCCTTTATTTGC         900           QY         901         CAACTTCATGTAGCTGTTGATTCAGAAATATTATTTGTAGCTATAGATTGTTACCTTTAT         960           DD         901         CAACTTCATGTAGGTTGATTCAGAAATATTATTTGTAGCTATAGATTGTTACCTTTAT         960

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0; Mismatches 278;
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HKYPSALHPKALSVNINKQIMDIYFKELLPLFVKPGDDGNYPSTAASDLACLQALSRR
IHYGKFVAEVKRADAPQDYEPAIRAQDREALMKLIFFEKVEEMVKKRVQKKAETFGGS
VKFNGSYGDSKKKYKYKDPLLASRIYGEMLIPLTKL
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protein id="AAM91774.1"

db_xref="G1:22136660"

/translation="MARVFESDSGSGCSNVLSLDLIRESLIRQEDTIVFSLIERAKFP

/translation="MARVFESDSGSGCSNVLSLDLIRESLIRQEDTIVFSLIERAKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-JUL-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arbhidopsis Pull-Length CDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satcu, M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAS: Yamada, K., Chang, M., Chang, C.H., Dale-J.M., Hauan, V.W., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, B.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Farlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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/db_xref="taxon:3702"
/chromosome="5"
/clone="U18739"
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681 665 735 795 785

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FEATURES

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Sequence 9 from patent
AR236640
AR236640.1 GI:27280726
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Boyes,D.C., Davis,K.R., Woessner,J.P., Gorlach,J., Hamilton,C.M.,
Hoffman,N.E., Kloti,A.S., Zayed,A. and Ascenzi,R.A.
Methods and compositions for the modulation of chorismate synthase
and chorismate mutase expression or activity in plants
Patent: US 6465217-A 3 15-OCT-2002;
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Boyes, D.C., Davis, K.R., Woessner, J.P., Gorlach, J., Hamilton, C.M., Hoffman, N.E., Kloti, A.S., Zayed, A. and Ascenzi, R.A.
Hoffman, N.E., Kloti, A.S., Zayed, A. and Ascenzi, R.A.
Methods and compositions for the modulation of chorismate synthase and chorismate mutase expression or activity in plants
Patent: US 6465117-A 9 15-OCT-2002;
Location/Qualifiers
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Pred. No. 4e-66;
0; Mismatches 2
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/mol_type="genomic DNA"
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Mulpuri, R. and Kjemtrup, S.
Methods and compositions for the modulation of chorismate synthase and chorismate mutase expression or activity in plants
Patent: WO 0202798-A 3 10-JAN-2002;
Paradigm Genetics Inc. (18)
Location/Qualifiers
1. 1006
/organism="Arabidopsis thaliana"
//mol.type="unassigned DNA"
//db_xref="taxon:3702"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                   429 CTGGGATATTTACTTTAAAGAATTGCTTCCTTTGTTTGTCAAACCTGGCGATGATGGCAA
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HYOKFVAEVKRDAPQDYEPAIRAQDREALMKLLIFEKVEEMVKKKVÇKKAETFGQE
VKFNGGYGDESKKKYKUPLIASRIÝGEWLIPLIKLVENEYEYLIRRD"
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                               CATCTACGGGGAATGGCTTATCCCTCTCACTAAGCTCGTTGAGGTTGAGTATCTTCTACG 159
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  <u> aagagretregaareggarreggirerggirerregargreraggerergaerraar</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Badur, R., Gaiger, M., Kunze, I. and Sommer, S.
Changing the fine chemical content in organisms by genetically modifying the shikimate pathway
Patent: WO 0200901-A 3 03-JAN-2002;
Sungene GmbH & Co. KgAA (DE)
Location/Qualifiers
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                                         CTTGTACAAAATTGGGTGATACCTCTCACCAAGGAGGTTCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:3702"
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/db_xref="GI:18491973"
                                                                                                                                                                                                                                                                     AX343933 1006 bp Sequence 3 from Patent WO0200901.
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rcgrcrcgarrgaa 145
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1006 bp mRNA linear PLN 13-AUG-1999
Arabidopsis thaliana chorismate mutase mRNA, complete cds.
147355
L47355.1 GI:5732015
Arabidopsis thaliana (thale cress)
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                                                                                                                                                           AAGAGTCTTCGAATTCGGGTTCTGGTTCCAATGTACTGAGTCTTGACTTAAT
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                                                                                                                             AATGGCCAAAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGT
                                                           Score 327.2; DB 6;
Pred. No. 4e-66;
0; Mismatches 278;
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                              32.1%;
Similarity 64.2%;
0; Conservative
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Methods and compositions for the modulation of chorismate synthase and chorismate mutase expression or activity in plants
Patent: WO 0202798-A 9 10-JAN-2002;
Paradigm Genetics Inc. (US)
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Arabidopsis thaliana
Bukaryota, Virighlantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                              CAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAAATTTACCACCATCAATTGTGCCATC
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                                               GITICCACTCAATICICCTGCTTTTCGAGGAATCTCGTTGTCTAGATTCTGGAAGTTTCTC
                                                                                                                                                                          rgaaracccggaagaarccrrrcrrcrrcaagaacarrccrcacrcggrrrrrccrac
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                                                                                                                                                                                                                                369 GCACAAATATCCATCGGCTTTGCACCCTAAGGCTCTATCTGTTAACATTAACAAAAT
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Sequence 9 from Patent W00202798.
AX464581 GI:21899376
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", Sakano, H., Pham, P.K., Banh, J., Chung, M.K., J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., T., Cheuk, R., Hayshizaki, Y., Ishida, J., K., Kayashizaki, Y., Ishida, J., Katlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Shinn, P., Southwick, A., Shinozaki, K., and Theologis, A.
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J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Yamamura, Y., Yu, G., Yu, S., Bowser, L.,
I., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
J., Seki, M., Shinn, P., Southwick, A.,
K.W., Ecker, J.R. and Theologis, A.,
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94710, USA
cciences Contact (GSC) members carried out the
stering of RAFL cDNAs (RAFL cDNA: 'RIKEN
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A. Shinozaki,K.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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CTATCCATCAACTGCTGCTAGTGATCTCGCCTGTTTACAAGCTCTTTCGAGAAGGATTCA
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use Patent: WO 0216655-A 972 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations A (CH)
                                                                                  CTATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGCTCCTCAAGACTACGAGCCTTT
                                                                                                                 644 GATTCGCGCTCAGGATAGAGAGGCTTTGATGAAGCTGTTGACGTTTGAGAAGTAGAAGA
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/organism="Arabidopsis thaliana"
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  Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamH1/XhoI insert."
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.larity 64.2%; Pred. No. 4e-66;
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/codon_start=1
/product=mutative chorismate mutase CM2"
/protein_id="AAL38714.1"
/db_xref="GI:17529008"
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/replace="t"
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/mol_type="mRNN"
/do_xref="taxon:3702"
/chromosome="5"
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       CAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAAATTTACCACCATCAATTGTGCCATC
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IBRAKFPLMSPAFEESRCLDSGSFSSLTEFFVRETEI LQAKVGRYEYPEBNPFFLENI
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LQALSRRIHYGKFVARVFREDAFPOYPEPA TRAQDERALMKLLFFEKVEEMVKKRVQKK
AETFGQEVKFNSGYGDESKKKYKVDPLLASRIYGEWLIPLTKLVEVEYLLRRLD"
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Pred. No. 6.8e-66;
0; Mismatches 278; Indels
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527 TCTAGAAGGATTCACTATGGAAAATTTGTTGCTGAAGTTAAATTTAGAGATAGTATTGAT
                                                                                                  508 ACAAGCGTTGAAGACGCTGAGGAAGAGTTGAAAAGAAGGCTGTGGTGTTTGGGCAG
                                                                                                                  GAAGTGAATCTTAACAGTGATGACAATGACAATGAAAACCGTAAATTTGATCCATCAGTG
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Unclassified.

(Modes 1 to 1231)

Falco, S.C., Famodu, O.O. and Lee, J.-M.
Aromatic amino acid biosynthetic enzy
Patent: US 667798-A 13 30-SEP-2003;
Location/Qualifiers
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AR404687
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/mol_type="genomic DNA"
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QLPBSSNFSGSLFQYLRQETBSLQSKYGRYLAPERNPFPDNLSDSIIPLTKCTPVLH
PAAESVNVNJEXILDIYINQMLPLFCTEVNDDANFATTAACDIQLLQALSRRIHYGKFV
AEVKREDSIDEYKPFILAQDRALMKLLIFBAYERNYKKRAAKKAKKGQEVSLADNA
EEVKGKIDPLLVSRLYDEWVMPLTKLVEVEXLLRRLD"
                                                                            Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. (bases 1 to 1000)

Eberhard, J., Blaschoff, M., Raesecke, H.R., Amrhein, N. and Schmid, J. Isolation of a cDNA from tomato coding for an unregulated, cytosolic chorismate mutase
perform Mol. Biol. 31 (4), 917-922 (1996)
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0; Mismatches 257; Indels 6;
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// "Organism="Lycopersicon esculentum"
//mol_type="mRNA"
/srrain="UG82b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="chorimate mutase"
/protein_id="AAD48923.1"
/db_xref="GI:5732018"
                                     chorimate mutase; mutase.
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:4081"
/clone="cLeCM2"
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/EC_number="5.4.99.5"
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Full Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Full Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Full Genome, Y., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kusumagi, T., Lu, M., Masuda, H., Miutra, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, R. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Haraoka, T., Hara, A., Hashizume, W., Hashizume, W., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Immura, K., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kanagawa, S., Kanolo, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kishikawa-Hirozane, T., Noilma, Y., Kondo, S., Konno, H., Kawai, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Shazaki, A., Sakai, C., Sakatume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata
                           Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayami, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayami, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kondo, S., Konno, H., Kouda, M., Matsuyama, T., Mura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nabi, K., Nowura, M., Namiki, T., Narikawa, K., Mikura, J., Nishi, K., Nowura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Cora, Y., Ctomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sainagawa, A., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Sugawa, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Tanaka, T., Tomaru, A., Taya, T., Yaundda, Y., Udda, M., Waki, K., Xie, Q., Yahagi, W., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Η.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Submitted (05-DEC-2001) Shoshi Kikuchi, Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-8602, Japan (E-mail:sKikuchi@mias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
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Pred. No. 8.9e-50;
0; Mismatches 331;
Kawagashira, N.,
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Best Local Similarity
Matches 469; Conserv
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us-10-624-061-15.rge

5 TITGCTACAATGCTGATATATGATAAAATGCTTTCCATGTGGATGGA	S AGAGCCTGATGACACCCATTCTTCGGAGGATCTGCCTGAACCACTGTTGCCACCTC 544  4 ACTCCTTCAAACGTTTTTGCATCCTGGTGCTGCTTCAATTAACATAACAAGAGTCCATCT 383  5 TCCAGTATCCAAAGAGTTTTGCATCCTATTGCTGATTTAATATCAACAAGAGAGATTT 604  4 GGAAAATGTATTTCAAAGAGTTACTTCCATTGCTTACTTCGGGTGATGATGGCAACT 443	4 AIGGGAAACTGCAGCTAAIGACCTTCATTATTGCAGTCCATCTCTAGAAGGATTCACT 503			1 TAGACTGAAGGCATTACAATGCA 823 
365 TTTGC 204 CATTGC         425 CTTTGC 264 AAAACC	485 AGAGC 324 ACTCC 545 TCCAG 384 GGAAAA 605 GGAAAA.	444 ATGCG     665 ATGGA 504 ATGGA      725 ATGGTI	564 TTCGA(   1 785 TAATA( 624 CGGTG)   1 845 CTATTO	684 GTGATO         905 CTGAAO 741 ACAAAO 965 ACAGC	801 TAGAC      1025 TGGAT
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Search completed: September 25, 2004, 00:33:08 Job time: 4169 secs

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1; Search time 477 Seconds (without alignments) 9084.197 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 US-10-624-061-15 Perfect score: Scoring table: Sequence:

Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues Searched:

6747726

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 2000000000 DB Minimum Maximum Maximum M

N Geneseq 29Jan04:\*
: geneseqn1980s:\* geneseqn2001bs:\* geneseqn2002s:\* geneseqn2001as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* geneseqn2003as: geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aba91394 Abz13167 Aba99614 Abx93057 ABA91394 ABZ13167 ABA99614 ABX93057 AAC33324 ABA91393 Length DB Query 23.05.05 23.05.05 23.05.05 23.05.05 24.05 254.8 Result No.

96 52 02 02	Aaf14469 Aspergill Abt17891 Aspergill Abt19705 Aspergill Aah44222 Physocomit	m 0 m	Abl34175 Human imm Abl33676 Human imm Abl34576 Human met Abl70369 Chemicall Abl22866 Human imm	4.00 Q W 4.0
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9777	W L L 4	767	ωωωωω	7000000
5099 552 601	2965 2980 7987 567	2000 4149 2000	113515 5379 5379 5379 5379 6219	6219 5311 7455 6418 6418
2.00 1. 60	4446	<i>-</i>	64446	444 W W W
60.40	0 0 0 <del>4</del>	6 4 4	4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4	w 44 44 w w w
7 6 2 5 4	3000	2 6 4	98788 9879	4 4 4 4 4 4 0 4 2 2 4 2
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# ALIGNMENTS

Soybean, plant, gene, ss, chorismate mutase, aromatic amino acid, diet, biosynthesis, chorismate, anthranilate, tryptophan, prephenate, tyrosine, phenylalanine, prephenate dehydrogenase, herbicide, food crop. ABX93058 standard, cDNA, 1020 BP Soybean chorismate mutase cDNA. (first entry) Glycine max. 22-MAY-2003 ABX93058; RESULT 1 ABX93058 

"Chorismate Location/Qualifiers 23. .808 /\*tag= a /product= "Chorismate Key

mutase"

US2002184658-A1

99US-00454279. 98US-0110845P. FALC/) FALCO S C. FAMO/) FAMODU O O. LEEJ/) LEE J. 04-DEC-1998; 03-DEC-1999; 05-DEC-2002.

Lee J; Falco SC, Famodu OO,

WPI; 2003-328651/31. P-PSDB; ABU08094.

New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.

Claim 3; Page 22; 32pp; English.

Arabidops

The invention discloses isolated polynucleotides encoding chorismate

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TGGGCAGGAAGTGAATCTTAACAGTGATGACAATGAAAAAAACCGTAAATTTGATCC 720
                                                                                                                                                                                       CAACTICATGIAGCIGITGATICAGAAATAITAITIGIAGCIATAGATIGITACCITTAI 960
                         ATCAGTGGCTTCTAGCTTGTACAAAATTGGGTGATACCTCTCCCCAAGGAGGTTCAGGT
                                                                               TGAGTACCTCTTGCGCCGTCTAGACTGAAGGCATTACAATGCAGTTAGAATTTAGAAGAA
                                                                                                  TGAGTACCTCTTGCGCCGTCTAGACTGAAGGCATTACAATGCAGTTAGAATTTAGAAGAA
                                                                                                                                                             regaagargarargargrrerreraaargarraagcrerraagrgarecritaarree
                                                                                                                                                                                                             CAACTICATGIAGCIGITGATTCAGAAATATTATTTGIAGCTATAGATTGITACCTTAT
                                         IGTICAAATGATTAAGCTCTTAAGTGATCCTTTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean chorismate mutase expressed sequence tag.
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/product= "Chorismate mutase"
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                                                                                                                                    TGGAAGATGATATGATGTTGT
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                                                                                                                                                                                                                                                                                                                                            ABX93053 standard; cDNA; 525
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FAMODU O O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-328651/31.
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(FAMO/) FAMODU (
(LEEJ/) LEE J.
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  converted to anthranilate amino acids must be included in the diets of animals. In the arcmatic amino acid biosynthetic pathway chorismate is converted to anthranilate during tryptoplan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymucleotide that affects the level of expression of a tyrosine plyspetide in a host cell, obtaining a mucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme plypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of these enzymes may be used to increase the content of aromatic amino acid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used to design and/or incline acids may be used to create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits linked to those genes. The sequence presented is a soybean chorismate
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Soybean, plant, gene, ss, chorismate mutase, expressed sequence tag, EST, aromatic amino acid, diet, biosynthesis, chorismate, anthranilate, tryptophan, prephenate, tyrosine, phenylalanine, prephenate dehydrogenase, herbicide, food crop. The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets New tyrosine biosynthetic enzyme, chorismate dismutase, proteins ar nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for

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of animals. In the aromatic amino acid biosynthetic pathway chorismate is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymucleotide that affects the level of expression of a tyrosine biosynthetic enzyme polypeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and ryrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good these enzymes may be used to increase the content of aromatic amino of these enzymes may be used to increase the content of aromatic amino acid in food crops. The polypeptides may also be used as herbicides. The nucleic acids may be used to create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits matter animals.
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TCAATTGTGCATCTTACTCCTTCAAACAGTTTTTGCATCCTGGTGCTGCTTCAATTAAC 360 427 487 ACGCTAGCTTCTGTGAGAGAGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC 127 ATTGAGAGAGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAAGTATGCTCAAATC 187 AAGGCTGGAAGATATACAAAAACCTTCTTCCCAGAAAATTTACCACA 307 TCAATTGTGCCATCTTACTCCTTCAAACAGTTTTTGCATCCTGGTGCTGCTTCAATTAAC 367 GGTGATGATGGNAACTATGCGCAAAACTGCAGCTAATGACCTTCATTATTGCAGT-CATC 479 61 ACGCTAGCTTCTGTGAGAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTAAGAATACAGAGGCCATTCAAGCT CAGGGTTTTTGTGGCTCATTGGTGGAATTGTTGTTAAGAATACAGAGGCCATTCAAGCT 8 AGCTTAATTTCAAGAATGGCCAAAAGCAGAACAAAGTCCTGATTCTGGGAATGTGTAC GGTGATGATGGCAACTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCAGTCCATC Gaps 2; Length 525; Sequence 525 BP; 160 A; 103 C; 111 G; 148 T; 0 U; 3 Other; 22; Indels Score 465.6; DB 7; Pred. No. 9.5e-117; 0; Mismatches 22; Query Match
Best Local Similarity 95.4%;
Matches 499; Conservative C Н 89 128 248 361 188 181 308 301 368 428 241 421

247 240

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TCTAGAAGGATTCACTATGGAAAGTTTGTAGCTGAGGTGAAAT 530
           TCTAGAAGGA-TCACTATGGAAAGTTTGTAGCTGANGNGAAAT
                                                       BP.
                                                      ABA99613 standard; DNA; 1006
                                                                                     entry)
                                                                                     (first
                                                                                     17-MAY-2002
 488
                                                                      ABA99613;
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DNA.

mutase-2

A. thaliana cytosolic chorismate

This invention describes a novel method for the preparation of fine chemicals by culturing organisms in which the shithmate pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutage and/or transcription or translation in plants. The method is used to produce chemicals, particularly Vitamins E or K and/or ubiquinone, useful e.g. also aromatic amino acids, salicylic or folic acid derivatives, but also aromatic amino acids, salicylic or folic acid derivatives, but plants with increased Vitamin E contents have improved resistance to plants with increased Vitamin E contents have improved resistance to abiotic stress, e.g. frost and drought. Transgenic plants Also plants with increased Vitamin E contents have improved resistance to shikimate pathway are useful as foods, fodder and in preparation of processed foodstuffs. Transgenic plants with modified shikimate pathways are useful as goods, fodder and in preparation of processed content of desired chemicals, particularly tocopherols and/or tocotrienols. This sequence encodes the Arabidopsis thaliana cytosolic chorismate mutase-2 protein used in the method of the invention Shikimate pathway, chorismate mutase, gene, prephenate dehydrogenase, vitamin E, vitamin K, ubiquinone, fat-soluble antioxidant, transgenic, feed, pharmaceutical, cosmetic; aromatic amino acid; salicylic acid; folic acid; phenylpropacid; flavanoid; plant; abiotic stress resistance; tocopherol; tocotrieol; ds. Preparing fine chemicals, particularly Vitamins B and K, useful as antioxidants e.g. in foods or medicine, by growing organisms with altered Location/Qualifiers 64. 861 /\*tag= a /product= "chorismate mutase-2" Sommer S; Disclosure; Page 57-60; 74pp; German. antioxidants e.g. in foods or m shikimate biosynthesis pathway. (SUNG-) SUNGENE GMBH & CO KGAA Kunze I, 29-JUN-2000; 2000DE-01030647. 21-DEC-2000; 2000DE-01064454. 28-JUN-2001; 2001WO-EP007391 Arabidopsis thaliana Geiger M, 2002-164442/21 P-PSDB; AAM49654 WO200200901-A1. 03-JAN-2002 Badur R, WANTED THE PROPERTY OF THE PRO

DB 6; Length 1006; Sequence 1006 BP; 290 A; 188 C; 226 G; 302 T; 0 U; 0 Other; 32.1%; Score 327.2; DB 6; Length 64.2%; Pred. No. 7.4e-79; ive 0; Mismatches 278; Indels Local Similarity 64.2 es 510; Conservative Query Match Best Loca Matches

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Gaps

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128 141 201 248 261 81 69 AAGAGICTICGAATCGGATTCGGGTTCTGGTTGTTCCAATGTACTGAGTCTTGACTTAAT 82 GAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTCATTGAGAGGCCAA 189 GTTTCCACTCAATTCTCCTGCTTTCGAGGAATCTCGTTGTCTAGATTCTGGAAGTTTCTC 202 CICATIGGIGGAATIIGIIGIIAAGAAIACAGAGGCCAIICAAGCIIAAGGCIGGAAGAIA 22 AATGGCCAAAGCAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGT 142 GITCCCTAGCAATTCTCACACCTATGATGAAAGTATGCTCAAAATCCAGGGTTTTTGTGG 셤 셤 ð ò ò ठे

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TICTCTCACTGAGTTTTTCGTCAGAGAGACAGAAATCATCCAAGCTAAGGTAGGAAGATA
                                                                                                                                                                                                                                                                       CTACGGTAAATTTGTAGCTGAGGTCAAATTCAGAGATGCTCCACAAGATTACGAGCCTGC
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                           CAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAATTTACCACCATCAATTGTGCCATC
                                                   rgaaracccogaagaarccrircircrrgagaacarrccrcacrcogrirrirccrac
                                                                                CTGGAAAATGTATTCAAAGAGTTACTTCCATTGCTTGCTACTTCGGGTGATGATGCCAA
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Woessner JP, Gorlach J, Hamilton CM;
, Zayed A, Ascenzi RA, Allen K, Mulpuri R;
                                                                Arabidopsis chorismate mutase-2 antisense polynucleotide.
                                                                             enzyme; plant; antisense;
                 ВБ.
                                                                                                                                                                            (PARA-) PARADIGM GENETICS INC.
                 DNA; 1006
                                                                                                                                             22-JUN-2001; 2001WO-US020104
                                                                                                                                                             2000US-00610040
                                                (first entry)
                                                                                                                                                                                           Davis KR, W
Kloti AS,
                                                                                mutase-2;
                                                                                              Arabidopsis thaliana
                 standard;
                                                                                                              WO200202798-A2
                                                                                                                                                            05-JUL-2000;
                                                08-APR-2002
                                                                                                                              10-JAN-2002
                                                                                                                                                                                                   Hoffman NE,
Kjemtrup S;
                                                                                Chorismate
          1400/c
ABA91400
                                 ABA91400;
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278

WPI; 2002-154754/20

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The present sequence is that of an antisense oligonucleotide that is specific for Arabidopsis thaliana chorismate-mutase-2 (CM) mRNA. CM catalyses the conversion of chorismate to prephenate in a branch of the shiximate pathway leading to phenylalanine and tyrosine biosynthesis. It is essential for plant growth, inhibition of CM gene expression in plant seedlings results in severe chlorosis, redeiced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense and sense polynucleotides, double-stranded RNA and ribozymes, and related expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that produce seedless fruit
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Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
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                  Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
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                                                                                                                                                                   249 Trcrcrcacreagritiricercagagadadagaartcarccaagcraagaragaagara
                                                                                                                                                                                                                                                                                                  322 ITACTCCTTCAAACAGTTTTTGCATCCTGGTGCTTCAATTAACATAAACATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana stress regulated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       849 TCGTCTCGATTGAA 862
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22 AATGGCCAAAGCAGCAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGT

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This invention describes a novel method for the preparation of fine enhericals by culturing organisms in which the shikinate pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutase and/or prephenate dehydrogense, linked to at least one regulatory sequence for transcription or translation in plants. The method is used to produce chemicals, particularly Vitamins B or K and/or ubiquinone, useful e.g. as alta-soluble antioxidants (in feeds, pharmaccuticals and cosmetics), but phenylpropanoids, flavanoids etc., especially in transgenic plants. Also plants with increased Vitamin B contents have improved resistance to abiotic stress, e.g. frost and drought. Transgenic plants with an altered shikimate pathway are useful as foods, fodder and in preparation of
605
                                                                                                                                                                                               735
                                                                                                                                                                                                                                                          725
                                                                                                                                                                                                                                                                                                                                                                                           785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shikimate pathway, chorismate mutase, gene, prephenate dehydrogenase, vitamin E, vitamin K, ubiquinone, fat-soluble antioxidant, transgenic, feed, pharmaceutical, cosmetic, aromatic amino acid, salicylic acid, folic acid, phenylpropanoid, flavanoid, plant, abiotic stress resistance, tocopherol, tocotrienol ds.
546 GATTCGCGCTCAGGATAGAGAGGCTTTGATGAAGCTGTTGACGTTTGAGAAAGTAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                           <u>carchaceegaareectrarecerereachaaeereerreachaaerreach</u>
                                                                                                                                506 AATGGTTAAGAAGAGAGTGCAGAAGAAGCAGAAACGTTTGGACAAGAAGTAAAATTCAA
                                                                                                                                                                                               -----CAGTGATGACAATGACAATGAAAACCGTAAATTTGATCCATCAGTGGCTTCTAG
                                                                                                                                                                                                                                                          666 crcreecrariecceareaegaagaagaagaagrariaaagreearcearrecrreecree
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                                                                  522 GACGGTGAGGAAGAGTTGAAAAGAAGGCTGTGGGTGTTTGGGCAGGAAGTGAATCTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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21-DEC-2000; 2000DE-01064454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing production of transgenic plants, cells and seeds and in producing with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501
                                                                                                                                                                                                                                                                                                                                                            Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 144; SEQ ID NO 972; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 798 BP; 223 A; 162 C; 180 G; 233 T; 0 U; 0 Other;
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                                                                                                                             (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                  Wang X,
                                  26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
   24-AUG-2000; 2000US-0227866P.
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Best Local Similarity 64.2
Matches 509; Conservative
                                                                                                                                                                                                                                     Harper JF, Kreps J,
                                                                                                                                                                                                                                                                                                 WPI; 2002-304127/34.
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q ò Rice; plant; gene; ss; chorismate mutase; aromatic amino acid; diet; biosynthesis; chorismate; anthranilate; tryptophan; prephenate; tyrosine; phenylalanine; prephenate dehydrogenase; herbicide; food crop.

Rice chorismate mutase cDNA

22-MAY-2003

/\*tag= a /product= "Chorismate mutase" 'note= "No start codon shown"

'partial

Location/Qualifiers 253. .1026

Oryza sativa

Key

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have increased content of desired chemicals, particularly tocopherols and/or tocotrienols. This sequence encodes the construct pCR-Script/AtCM-ITP-ATCM-2 which is composed of the Arabidopsis thaliana plastid chorismate mutase-1 transit poptide and a Arabidopsis thaliana chorismate mutase-2 fragment and is used for plastid localisation
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                                                                                                                                       DB 6; Length 993;
                                                                                                         Seguence 993 BP; 259 A; 227 C; 210 G; 297 T; 0 U; 0 Other;
                                                                                                                                    tch 32.0%; Score 326.2; DB 6; Length al Similarity 64.2%; Pred. No. 1.4e-78; 509; Conservative 0; Mismatches 278; Indels
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New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for

producing antibodies.

Lee J;

Falco SC, Famodu 00,

(FALC/) FALCO S C. (FAMO/) FAMODU O O. (LEEJ/) LEE J.

WPI; 2003-328651/31. P-PSDB; ABU08093.

98US-0110845P. 99US-00454279

04-DEC-1998; 03-DEC-1999;

05-DEC-2002

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The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of onverted to anithranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine converted to prephenate. Also disclosed are methods for selecting an isolated polympetide are methods for selecting an isolated conjustification of a tyrosine polympetide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme polypeptide can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of these enzymes may be used to increase the content of aromatic amino acid in food crops: The polypeptides may be used to design and/or identify inhibitors of those enzymes that may be used as herbicides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identify inhibitors of those argames that may be used as herbicides. The mucleic acids may be used to create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits linked to those genes. The sequence presented is a rice chorismate mutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 TGGCCAAAGCAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1231 BP; 352 A; 276 C; 311 G; 292 T; 0 U; 0 Other;
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58.4%; Pred. No. 9.1e-60;
iive 0; Mismatches 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 20-21; 32pp; English
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8
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BP.

ABX93057 standard; cDNA; 1231

RESULT 8 ABX93057 ID ABX9

QQ	239 TGACCAAGGAGAAAAAAGAGATAGATCAAAGTGAAATACTGACCTTGGACAACATTA 298	XGX	06-SEP-2000.		
ò	84 GAGAGGATITGGTIAGGCAAGAGGATACCATTATGGTCTCAITGAGAGAGCCAAGT 143	F X	25-FEB-2000;	2000EP-00301439.	
qq	AGGCAAGAAGACAGCATCATATTCAGCCTCTTAGAGAGA	P. 9.	25-FEB-1999;	99US-0121825P.	
ò	144 TCCCTAGCAATTCTCACACCTATGAAAAGTATGCTCAAATCCAGGGTTTTTGTGTGGCT 203	. K. E	9-MAR-19	99US-0123548P.	
Op	359 TTTGCTACAATGCTGATATATATGATAAAATGCTTTCCATGTGGATGGA	. C. C	5-MAR-19	99US-0126264P.	
ò	204 CATTGGTGGAATTTGTTAAGAATACAGAGGCCATTGAAGCTAAGGCTGGAAGATACA 263	ኛ ፫ (	1-APR-19	99US-0127462P.	
Ωp	419 CTITGGTTGAATTCATGGTTAGAGAAACGGAAAAACTACATCAACAGGTTGGGAGATACA 478	¥ ¥ £	08-APR-1999; 08-APR-1999;	99US-U128234F. 99US-0128714P. 00HS-012004ED	
ć	264 AAAACCCTCAAGAAAACGCCTTCTTCCCAGAAATTTACCACCATCAATTGTGCCATCTT 323	ኛ <b>ፎ</b> የ	9-APR-19	99US-0129045F.	
QQ	479 AGAGCCCTGALGACCCCATTCTTTCCGGAGGATCTGCCTGAACCACTGTTGCCACCTC 538	ሟ	1-APR-19 3-APR-19	99US-0130449F. 99US-0130510P.	
ò	324 ACTCCTTCAAACAGTTTTTGCATCCTGGTGCTTCAATTAACATAAAGAAGTCCATCT 383	<u>ኛ</u> ፎ !	3-AFK-19 8-APR-19	99US-013U89IF. 99US-0131449F.	
Dp	539 TCCAGTATCCAAAGGTTTTGCATCCTATTGCTGATTCTATTAATATCAACAAGGAGATTT 598	0, 0, X X X	0-APR-19 0-APR-19	99US-0132048F. 99US-0132407F.	
à	384 GGAAAAIGIAITICAAAGAGITACTICCAITGCTIGCTACTICGGGIGAIGAIGGCAACT 443	ሟ ያ	4-MAY-19 5-MAY-19	99US-0132484P. 99US-0132485P.	
Db	599 GGAAAATGTATTTTGATGAGCTTCTTCCAAGATTAGTGAAAGGAAGG	¥ ¥	6-MAY-19 6-MAY-19	99US-U132486F. 99US-0132487F.	
ઠે	ATGCGCAAACTGCAGCTAATGACCTTT	ሟ ሟ ሟ ሟ	7-MAY-19 1-MAY-19	99US-0132863P. 99US-0134256P.	
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S 1		. A. E	8-MAY-19	99US-0134768P.	
on .	AIGGIAAGITTGTGGCAGAGGTAAGTTTCAAGAGTCTCCTGAAGCTAACATGCCTGCGA	7 T T	0-MAY-19	99US-0135124P.	
à	TTCGAGCTAAGGATAAAGAATGGAATTGTTGATAAATTTACAAGCGTTGAAGAGA 52.	<u>ኛ</u> ዊ	1-MAI-19 4-MAY-19	99US-0135629P.	
Op	779 TAATAGCACAGGACTGCGATCAACTAATGCACCTCCTCACCTATGAAACGGTGGAGCGTG 838	<u>ጽ</u>	5-MAY-19 7-MAY-19	99US-0136021P. 99US-0136392P.	
Š	624 CGGTGAGGAAGAGGTTGAAAGAAGGCTGTGGGCAGCAAGTGAAGTGAATCTTAACA 683	ሟ ሟ ፙ ፠	8-MAY-19 1-JUN-19	99US-0136782P. 99US-0137222P.	
qq	839 ctattgaacatagggtggaaggtaaggctaagatctttggacacagggggggg	전 전 전 전	3-JUN-19	99US-0137528P. 99US-0137502P.	
ò	684 GTGATGACAATGACAATGAAAACCGTAAATTTGATCCATCAGTGGCTTCTAGCTTGT 740	: K. E	19 - NUT - 7	99US-0137724P.	
Dp	899 CTGAAGACAACGCCCCCCCCACCATGTACAGATAAGGCCCAGTTTGGTGGCTGAACTGT 958	ያ <u>የ</u> የ		99US-0138540P.	
ò	741 ACAAAAATTGGGTGATACCTCTCACCAAGGAGGTTCAGGTTGAGTACCTCTTGCGCCGTC 800	ዊ ያ		99US-0138847P. 99US-0139119P.	
. d	ACAGCTACAGGATCATGCCGCTAACCAAGGAGGTTCAAGTAGCCTACTTGCTG	ሟ ሟ	16-JUN-1999; 16-JUN-1999;	99US-0139452P. 99US-0139453P.	
8	######################################	다. 보고 보고		99US-0139492F. 99US-0139454F.	
S 1		. K.		99US-0139455P.	
a a	1019 TGGATTGATTGTTACGATTGTA 1041	. E.		99US-0139457P.	
RESUI	6 E	ም የ የ		99US-0139458F. 99US-0139459F.	
AAC3.	324 AAC33324 standard; DNA; 1274 BP.	ጟ <b>፫</b> ፤	91-NDD-	99US-013946UF.	
¥ X	AAC33324;	ጃ <u>ዋ</u>	TO CO	99US-U139462F. 99US-0139463F.	
XX	-OCT-2	ዋዋ ዋዋ	8-NUV-19	99US-013975UP. 99US-0139763P.	
EX	abidopsis thaliana DN	ጟ <b>ଫ</b> የ	21-808-19 21-808-19	99US-U13981/F. 99US-0139899P.	
X X	bridisation assav: denetic mapping: gene expression	ማ ማ ጜ ጜ	3-JUN-19 3-JUN-19	99US-0140353P. 99US-0140354P.	
KKW	protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss	됐 <b>없</b>	$\mathbf{m} \cdot \mathbf{m} \cdot \mathbf{n}$	99US-0140695P. 99US-0140823P.	
X S	Arabidopsis thaliana.	ያ <u>ዋ</u> ይ	0-70N-19 0-70N-19	99US-0141287P.	
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68 ACGCTAGCTTCTGTGAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC 127 327 ACTCTTGAAGGTATTAGAAACTCTTTGATCCGTCAAGAGGACAGCATTATATATTTGGGCTA 308 TCAATTGTGCCATCTTACTCCTTCAAACAGTTTTTGCATCCTGGTGCTGCTTCAATTAAC 567 CCTATGTTGCCTCCTCTCAGTACCCAAAGGTGTTGCATTTTGCTGCTGATTCGATAAAC 248 AAGGCTGGAAGATACAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAAATTTACCACCA 627 ATABACAAGAAGATATGGAACATGTACTTCAGAGACCTTGTTCCAAGACTTGTGAAGAAA TCTAGAAGGATTCACTATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGCTCCTCAA CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTAAGAATACAGAGGCCATTCAAGCT 447 garddrircaarddricrirddriadaracarddriaaaggcacrdadaagcricacdcr 428 GGTGATGATGCCAACTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCAGTCCATC Gaps 23; Length 1274; 290; Indels Score 255; DB 3; Pred. No. 4.2e-59; 0; Mismatches 99US-0155139P.
99US-0155486P.
99US-015568P.
99US-015658P.
99US-015658P.
99US-015713P.
99US-015732P.
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99US-016098P.
99US-016098P. 59.6%; Query Match Best Local Similarity 59.6 Matches 462; Conservative 22-SEP-1999; 24-SEP-1999; 26-SEP-1999; 26-SEP-1999; 05-OCT-1999; 05-OCT-1999; 06-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 21-071-1999 21-071-1999 21-071-1999 22-071-1999 22-071-1999 25-071-1999 25-071-1999 26-071-1999 26-071-1999 26-071-1999 26-071-1999 26-071-1999 26-071-1999 26-071-1999 28-OCT-1999 29-OCT-1999 188 507 488 368 à 셤 g 엄 g 셤 ò δ 8 8 જે 원 à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
TCAAAGAGAATCCATTACGGTAAATTTGTTGCAGAAGCTAAATTTCAAGCCTCACCCGAA
                                                                         GCATACGAGTCCGCCATCAAAGCACAAGATAAGGATGCACTGATGGATATGCTGACATTC
                                                                                                       ACAAGCGTTGAAGAGGGGGAAGAGAGAGTTGAAAAGAAGCCTGTGGTGTTTTGGGCAG
                                                                                                                                  867 cegaereregaagarecearaaagaagaaerreagareaaaaeeegaacaraeeegaa
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                                            GACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTTGACATTT
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Mulpuri
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Ascenzi RA,
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Hoffman NE,
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provided for using CM in the identification of herbicide candidates. Methods are also provided for identifying compounds that stimulate the expression or function of CM. These can be used to promote growth and
                                                                                                                                                                                                                               ATTGAGAGAGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAAGTATGCTCAAATC
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0; Mismatches 342; Indels
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                                                                                                         Score 254.8;
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      ATABACAAGAAGATATGGAACATGTACTTCAGAGACCTTGTTCCAAGACTTGTGAAGAAA
                                                                                                                         <u> GGCGATGATGGTAACTACGGCTCAACAGCTGTCTGTGACGCTATCTGCCTTCAGTGTCTC</u>
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                                                                                    GGTGATGGTGGCAACTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCAGTCCATC
                                                                                                                                                                  TCTAGAAGGATTCACTATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGCTCCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana; plant; gene; stress; transgenic; ds
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                                                                                                                                                                                                                                                                                                                                                                                                              668 GAAGTGAATCTTAACAGTGATGACAATGACAATGAAAA----
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of an antisense oligonucleotide that is specific for Arabidopsis thaliana chorismate-mutase-1 (CM) mRNA. CM catalyses the conversion of chorismate to prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine biosynthesis. It sesential for plant growth; inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense and sense polynucleotides, double-stranded RNA and ribozymes, and related expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 ACGCTAGCTTCTGTGAGAGAGTTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 ATTGAGAGGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAAGTATGCTCAAATC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 895 TTGGAGAGGCCAAGTACTGTTACAATGCTGATACTTATGATCCTACTGCTTTTGACATG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 835 GATGGTTTCAATGGTTCTTTGGTTGAGTACATGGTTAAAGGCACTGAGAAGCTTCACGCT 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGTTGGTAGGTTTAAGAGTCCTGATGAACATCCTTTCTTCCCTGATGATCTACCAGAG 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 TCAATTGTGCCATCTTACTCCTTCAAACAGTTTTTGCATCCTGGTGCTGCTTCAATTAAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTAAGAATACAGAGGCCATTCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CM;
Mulpuri R;
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Pred. No. 4.6e-59;
0; Mismatches 342; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1207 BP; 354 A; 278 C; 232 G; 343 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamilton (
Allen K, N
                                                                                                                       Arabidopsis chorismate mutase-1 antisense polynucleotide.
                                                                                                                                                              Chorismate mutase-1; enzyme; plant; antisense; ss
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Ascenzi RA,
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Zayed A,
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  BP
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ABA91399 standard; DNA; 1207
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                                                                             (first entry)
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Kloti AS,
                                                                                                                                                                                                     Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                     10-JAN-2002
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Hoffman NE,
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 251; DB 6; Length 1005;
Pred. No. 4.7e-58;
0; Mismatches 285; Indels 2
                                                                 737; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1005 BP; 287 A; 205 C; 235 G; 278 T; 0 U; 0 Other;
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Local Similarity 59.6%;
Les 456; Conservative (
                                                                 SEO ID NO
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The invention discloses isolated polymuclectides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals: In the aromatic amino acids must be included in the diets of animals: In the aromatic amino acid biosynthesis and is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine converted to prephenate. Also disclosed are methods for selecting an isolated polymethetic enayme polypeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enayme polypeptide and ritiodics. Chorismate mutase ability to inhibit the activity of a tyrosine biosynthetic enayme polypeptide and entibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of these enaymes may be used to increase the content of aromatic amino of these maymes may be used to increase the content of aromatic amino dentify inhibitors of those enzymes that may be used as herbicides. The polypeptides may also be used as defined and vor identify and physical mapping of the genes and as markers for traits and a mutase mutase mutase and as markers for traits mutase mutase.
                                                                                                                                                                                                                                     Corn; plant; gene; ss; chorismate mutase; aromatic amino acid; diet;
biosynthesis; chorismate; anthranilate; tryptophan; prephenate; tyrosine;
phenylalanine; prephenate dehydrogenase; herbicide; food crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tyrosine biosynthetic enzyme, chorismate dismutase, proteins ar
nucleic acids, useful for facilitating design and/or identifying
inhibitors of those enzymes that may be used as herbicides and for
'note= "No start codon shown"
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3. .998
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                                                                                                        ABX93056 standard; cDNA; 1223
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P-PSDB; ABU08092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FALC/) FALCO S C.
(FAMO/) FAMODU O O.
(LEEJ/) LEE J.
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Sequence 1223 BP; 341 A; 284 C; 312 G; 286 T; 0 U; 0 Other;
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                                                             Score 239.4; DB 7;
Pred. No. 7.5e-55;
0; Mismatches 351;
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BP.
                  ABX93059 standard; cDNA; 780
                                                                           Wheat chorismate mutase cDNA
                                                        (first entry)
                                                        22-MAY-2003
                                     ABX93059
        ABX93059
ID ABX9
XX
AC ABX9
XX
DT 22-P
XX
DE Whee
RESULT
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prephenate; tyrosine; food crop.
diet;
amino acid;
Wheat, plant, gene, ss, chorismate mutase, aromatic a
biosynthesis, chorismate, anthranilate, tryptophan, j
phenylalanine, prephenate dehydrogenase, herbicide,
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Triticum aestivum

Key

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1. .624
*tag= a
product= "Chorismate mutase"
                                                                                      /note= "No start codon shown"
Location/Qualifiers
                                                                       partial
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US2002184658-A1

05-DEC-2002

99US-00454279 03-DEC-1999; 98US-0110845P 04-DEC-1998;

(FALC/) FALCO S C. (FAMO/) FAMODU O O. (LEEJ/) LEE J.

<u>ن</u> Lee Falco SC, Famodu OO,

WPI; 2003-328651/31. P-PSDB; ABU08095

New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.

Claim 3; Page 23; 32pp; English.

mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of animals. In the aromatic amino acid biosynthetic pathway chorismate is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymucleotide that affects the level of expression of a tyrosine biosynthetic enzyme polypeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and fragment encoding a tyrosine biosynthetic enzyme polypeptide and a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good attrobates for therbicides that will not affect animals, and overspression of these enzymes may be used to innorease the content of aromatic amino acid in food crops. The polypeptides may be used to correate transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits and overspression of the genetic and physical mapping of the genes and as markers for traits and the content of an wheat chorismate The invention discloses isolated polynucleotides encoding mutase cDNA

Sequence 780 BP; 256 A; 146 C; 169 G; 209 T; 0 U; 0 Other;

331 129 69 10 dagrictrodricegeaagcegaegrecrecaegecaagecregaegrerareaaageea 272 GAAGAAAACGCCTTCTTCCCAGAAAATTTACCACCATCAATTGTGCCCATCTTACTCCTTC 212 GAATTIGTTGTTAAGAATACAGAGGCCATTCAAGCTAAAGGCTGGAAGATACAAAAACCT Gaps Indels 18; DB 7; Length 780; Score 229.4; DB 7; Pred. No. 3.3e-52; 0; Mismatches 206; Query Match
22.5%;
Best Local Similarity 63.6%;
Matches 391; Conservative ( g G g ò à

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The present sequence is that of a full-length cDNA encoding Arabidopsis thaliana chorismate mutase-3 (CM), an enzyme that catalyses the conversion of chorismate to prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine biosynthesis. CM is essential for plant growth; inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense (see ABA91401) and sense polynucleotides, double-stranded RNA and ribozymes, and related polynucleotides and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that produce seedless fruit. CM is also a target for the identification of herbicide candidates. Methods are also provided for in the identification of herbicide candidates. Methods are also provided for identification of herbicide candidates. Methods are also provided for incompounds that stimulate the expression or function of CM. These can be used to promote growth and
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Sequence 15, Application US/09454279;
Patent No. 662798
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BBL299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT APPLICATION NUMBER: 60/110,845
EARLIER APPLICATION NUMBER: 60/110,845
FARLIER FILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
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100.0%; Score 1020; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-261;
Matches 1020; Conservative 0; Mismatches 0;
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
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| Patent No. 6627798
| GENERAL INFORMATION: A PAPLICANT: Falco, S. Carl
| APPLICANT: Famodu, Omolayo O. A PAPLICANT: Famodu, Omolayo O. TITLE OF INVENTION: AROMATIC AMINO FILE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES FILE REFERENCE: BB1299 US NA
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CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
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ORGANISM: Glycine max
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APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Jouglas
APPLICANT: Boyes, Jeffrey
APPLICANT: Woesner, Jeffrey
APPLICANT: Gorlach, Jorn
APPLICANT: Gorlach, Jorn
APPLICANT: Hamilton, Carol
APPLICANT: Hoffman, Neil
APPLICANT: Kloti, Andreas
APPLICANT: Kloti, Andreas
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
FILE REPERENCE: 9128-14
CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                61 ACCCTACCTTCTGTGAGAGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC 120
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                                                                                                                                    1 AGCTTAATTTCAAGAATGGCCAAAGCAGAACAAAGTCCTGATTCTGGGAATGTGTAC
                                                                                                                                                                                  68 ACCCTACCTTCTGTGAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC
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                                              Gaps
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  Length 525;
                                              Indels
                                                                                          8 AGCTTAATTTCAAGAATGGCCAAAGCAGCAGAACAAAGTCCTGATTCT
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Score 465.6; DB 4;
Pred. No. 1.9e-114;
0; Mismatches 22;
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US-09-610-040-3
Query Match
Best Local Similarity 95.4%;
Matches 499; Conservative
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US-09-610-040-3
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32.1%; Score 327.2; DB 4; Length 1006; 64.2%; Pred. No. 1.5e-77;

RESULT 4
US-09-610-040-9/c
Sequence 9, Application US/09610040
Patent No. 6465217
GENERAL INFORMATION:
APPLICANT: Davis, Keith
APPLICANT: Woesener, Jeffrey
APPLICANT: Woesener, Jeffrey
APPLICANT: Hodfman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Kloti, Andreas
APPLICANT: Zayed, Adel
APPLICANT: Zayed, Adel
APPLICANT: Zayed, Adel
APPLICANT: Zayed, Adel

este.

5-()<sub>2</sub>

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS;
; TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
; FILE REFERENCE: 9128.14
; CURRENT APPLICATION NUMBER: US/09/610,040
; CURRENT PILLING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-610-040-9 4 459 339 279 735 219 795 159 879 141 819 201 759 261 669 321 639 381 579 441 519 501 561 399 621 681 458 CTACGGTAAATTTGTAGCTGAGGTCAAATTCAGAGATGCTCCACAAGATTACGAGCCTGC CAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAAATTTACCACCATCAATTGTGCCATC 698 TGAATACCCGGAAGGAATCCTTCTTCCTTGAGAACATTCCTCACTCGGTTTTTCCTAC TTACTCCTTCAAACAGTTTTTTGCATCCTGGTGCTTCAATTAACATAAACAAGTCCAT 518 CHAICCAICAACHGCHGCHAGHGAICTCGCCHGITTACAAGCTCTITCGAGAAGGAITCA CTATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGCTCCTCAAGACTACGAGCCTTT crcreecrarideceargageagraagaagracaraaaagagecrcree AAGAGTCTTCGAATCGGATTCGGGTTCTGGTTGTTCCAATGTACTGAGTCTTGACTTAAT 878 CAGAGAATCGTTGATTAGGCAAGAAGACACCATCGTCTTCAGCTTGATCGAGAGAGCTAA 202 CICATIGGIGGAAITIGITATAAAATACAGAGCCATICAAGCTAAGGCTGGAAGATA CIGGAAAATGIAITICAAAGAGITACTICCATIGCTIGCTACTICGGGIGAIGAIGGCAA 562 AATTCGAGCTAAGGATAAAGAATGATGAAATTGTTGACATTTACAAGGTTGAAGA 398 garricgcgcrcaggaragagaccrrrcargaagcrgrrgacgrrrrgagaaagragaaga GACGGTGAGGAAGAGATTGAAAAGAAGGCTGTGTGTGGGCAGGAAGTGAATCTTAA -----CAGTGATGACAATGACAATGAAAACCGTAAATTTGATCCATCAGTGGCTTCTAG 22 AATGGCCAAAGCAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGT GAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTCATTGAGAGAGCCAA GTTCCCTAGCAATTCTCACACCTATGATGAAAAGTATGCTCAAAATCCAGGGTTTTTGTGG CTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCAGTCCATCTCTAGAAGGATTCA Gaps 9 Length 1006; Query Match 32.1%; Score 327.2; DB 4; Length Best Local Similarity 64.2%; Pred. No. 1.5e-77; Matches 510; Conservative 0; Mismatches 278; Indels CCGTCTAGACTGAA 809 TCGTCTCGATTGAA 382 622 682 278 218 964 158 442 502 736 262 322 938 82 142 818 g d 8 8 ò 8 g ð

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APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Keith
APPLICANT: Boyes, Zeith
APPLICANT: Woessner, Jeffrey
APPLICANT: Gorsaner, Jorn
APPLICANT: Gorsaner, Jorn
APPLICANT: Affren, Meil
APPLICANT: Affren, Meil
APPLICANT: Ascenzi, Robert
ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHASI
ITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
ITLE OF INVENTION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
ITMETHER PROBLEM OF THE METHOD OF CHORISMATE SYNTHASI
STATE OF INVENTION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
ITMETHER PROBLEM OF THE METHOD OF CHORISMATE SYNTHASI
SEQ ID NO 2
ITMETHER PROBLEM OF THE METHOD OF CHORISMATE SYNTHASI
                                                                                                                              959 ACAGCTACAGGATCATGCCGCTAACCAAGGAGGTTCAAGTAGCCTACTTGCTGAGGAGAT 1018
399 CTGAAGACAACGGCGCTCCACCAATGTACAAGATAAGGCCCAGTTTGGTGGCTGAACTGT 958
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                                                                    741 ACAAAAATTGGGTGATACCTCTCACCAAGGAGGTTCAGGTTGAGTACCTCTTGCGCCGTC
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Pred. No. 2.7e-58;
0; Mismatches 342;
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, ORGANISM: Arabidopsis thaliana
US-09-610-040-2
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al Similarity 57.4%;
494; Conservative
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Best Local S:
Matches 494
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                                                                        Sequence 13, Application US/09454279
Fatent No. 6627798
General INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SSPTWARE: Microsoft Office 97
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Pred. No. 5.5e-59;
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Best Local Similarity 58.4%;
Matches 469; Conservative
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ORGANISM: Oryza sativa
                            RESULT 5
US-09-454-279-13
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Sequence 11, Application US/09454279

Patent No. 6627798

GENERAL INFORMATION:

APPLICANT: Famodu, Comlayo O.

APPLICANT: Lee, Jian-Ming

TILE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES

FILE REFERENCE: BB1299 US NA

CURRENT APPLICATION NUMBER: US/09/454,279

CURRENT FILING DATE: 1999-12-03

SARLIER FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

SEQ ID NO 11

LENGTH: 1223
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CRGANISM: Zea mays
US-09-454-279-11
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APPLICANT: BOYES, Reith
APPLICANT: BOYES, Reith
APPLICANT: BOYES, Reith
APPLICANT: Hosesner, Jeffrey
APPLICANT: Hosesner, Jeffrey
APPLICANT: Hoffman, Neil
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                                                                                                                          733 gcaraccadrocarcaaagcacaacaaaaraaaraaarcaacaaraaraararaaraacaarac 792
                                                                                                                                                                                                     ACAAGCGTTGAAGAGACGGTGAGGAAGAGAGTTGAAAAGAAGGCTGTGGTGTTTGGGCAG 667
                                                                                                                                                                                                                                                                     793 ccgacrcrcgaagargcgaraaaaaagagarrcaagargaaacccgaacaracggcda 852
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                                                                                                                                                                                                                                                                                                                                                GAAGTGAATCTTAACAGTGATGACAATGAAAA------
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                                                       GACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTTGACATTT
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25.0%; Score 254.8; DB 4; Length 1
Best Local Similarity 57.4%; Pred. No. 2.7e-58;
Matches 494; Conservative 0; Mismatches 342; Indels
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Patent No. 6465217
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; ORGANISM: Arabidopsis thaliana
US-09-610-040-8
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US-09-610-040-8/c
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                                                                                                                                                                                                                                                                                                                                      212 GAATTTGTTGTTAAGAATACAGAGGCCATTCAAGCTAAGGCTGGAAGATACAAAAACCCT
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                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                          Score 229.4; DB 4;
Pred. No. 1.3e-51;
0; Mismatches 206;
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Patent No. 6465217
GENERAL INFORMATION:
                                                                                                                                                                                                                          Query Match
22.5%;
Best Local Similarity 63.6%;
Matches 391; Conservative
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Woessner, Jeffrey
                                                                                                                 TYPE: DNA ORGANISM: Triticum aestivum
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Hamilton, Carol
Hoffman, Neil
Kloti, Andreas
Zayed, Adel
  NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office
SEQ ID NO 17
LENGTH: 780
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                                                                                                                                                                GTGTACACGCTAGCTTCTGTGAGAGAGTTTGGTTAGGCAAGAGGATACCATCATTAT 121
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Patent No. 6627798
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Fee, Jian-Ming
TILE REPERINGE BAL299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER FILING DATE: 1999-12-04
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APPLICANT: Ascenzi, Robert TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS! TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS

Boyes, Douglas Davis, Keith Woessner, Jeffrey Gorlach, Jorn Hamilton, Carol Hoffman, Neil

Kloti, Andreas Zayed, Adel

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APPLICANT: Zayed, Adel
APPLICANT: Zayed, Adel
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHASE
TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
FILE REPERRICE: 9128.14
CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT APPLICATION DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                 TYPE: DNA; CRGANISM: Arabidopsis thaliana
US-09-610-040-10
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Pred. No. 9.1e-47;
0; Mismatches 316;
FILE REFERENCE: 9128.14
CURRENT PEPLICATION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1217
                                                                                                           TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 AAGTAGTCAAGAGAGAGTTGAGATCAAAGCCAGAATTTTTGGTCAAGACATAACGATTA
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                                                                                      81 TGAGAGAGTTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTCATTGAGAGAGCCA
                                                                                                                                                                       141 AGTICCCTAGCAATICTCACACCTAIGAAAAGTAIGCICAAATCCAGGGITITITGIG
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                                             Gaps
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ز
Length 1217;
                                           Indels
  Score 211.4; DB 4;
Pred. No. 9.1e-47;
0; Mismatches 316;
  Query Match
Best Local Similarity 56.5%;
Matches 414; Conservative
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Sequence 10, Application US/09610040 Patent No. 6465217 GENERAL INFORMATION:

RESULT 11 US-09-610-040-10/c

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APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Weith
APPLICANT: Borlach, Join
APPLICANT: Borlach, Join
APPLICANT: Hamilton, Carol
APPLICANT: Hamilton, Carol
APPLICANT: Ascenzi, Robert
APPLICANT: Zayed, Adel
APPLICANT: Ascenzi, Robert
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHASE
TILE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
FILE REFERENCE: 9128.14
CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 6
LENGTH: 5176
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                                                                                                                                                                           423 AAGAGAAGTAGAAGAAGGAAAGATATTTGGACAGAATGTCACTCT 469
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                                                                                                                            632 AAGAGAGTIGAAAAGAAGGCIGIGGIGITIGGGCAGGAAGIGAAICI
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                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09610040 Patent No. 6465217 GENERAL INFORMATION:
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Best Local S:
Matches 164
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                                                                                                                                                                                                         Sequence 7, Application US/09454279;
Sequence 7, Application US/09454279;
Patent No. 6627798
; GENERAL INPORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: AROMING
FILE REFERENCE: BAL299 US NA.
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT APPLICATION NUMBER: 06/110,845
EARLIER APPLICATION NUMBER: 60/110,845
SALLIER PILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 206.2; DB 4; Length 579; Pred. No. 1.7e-45; 0; Mismatches 163; Indels 0;
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   798 GTCTAGACTGAAG 810
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ORGANISM: Triticum aestivum
                                                               135 GACTGGATTAATG 123
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Best Local Similarity 65.1
Matches 304; Conservative
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FRAUDER:
NAME/KEY: unsure
LOCATION: (565)
FARUNER:
NAME/KEY: unsure
LOCATION: (577)
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US-09-454-279-7
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Pred. No. 4.2e-09;
0; Mismatches 108; Indels
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Job time : 102 secs
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Best Local Similarity 55.4%;
Matches 134; Conservative
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(522)
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us-10-624-0.

APPLICANT: Xloti, Andreas
APPLICANT: Zayed, Adel
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS
TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
FILE REFERENCE: 9128.14
CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT PILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SSOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
IENGTH: 5099
TYPE: nv.
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NAME/KEY: misc feature
LOCATION: (4049)...(4049)
COTHER INFERMATION: "n" indicates any nucleotide (A, C, T, or G)
US-09-610-040-5
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Zea mays
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US-09-454-279-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09454279;
Publication No. US20020184658A1;
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl;
APPLICANT: Famodu, Omolayo O.;
APPLICANT: Famodu, Omolayo O.;
APPLICANT: Lancdu, Omolayo O.;
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES;
FILER REFERENCE: BEL299 US M.;
CURRENT PILING DATE: 1999-12-03;
EARLIER PILING DATE: 1999-12-04;
NUMBER OF SEQ ID NOS: 22;
SOFTWARE: Microsoft Office 97;
LENGTH: 1020
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6 US-10-624-061-13

5 US-10-267-763-8

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10S-09-938-842A-737

10S-09-454-279-11

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Sequence 7639, Ap
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1: \cgn2_6/ptodata/1/pubpna/VS07 PUBCOMB.seq:*
2: \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
4: \cgn2_6/ptodata/1/pubpna/VS06_NEW PUB.seq:*
5: \cgn2_6/ptodata/1/pubpna/VS06_NEW PUB.seq:*
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14: \cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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; PRIOR FILING DATE: BARLIER FILING DATE: 1998-12-04 ; NUMBER OF SEQ ID NOS: 22 ; SOFTWARE: Microsoft Office 97 ; SEQ ID NO 15 ; LENGTH: 1020 ; TYPE: DNA ; ORGANISM: Glycine max US-10-624-061-15	Query Match Best Local Similarity 100.0%; Pred. No. 2.7e-264; Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 GCACGAGAGCTTAATTTCAAGAATGGCCAAAGCAGGAGAAGTCCTGATTCTGGGAA 60	QY         61 TGTGTACACGCTAGGTTCTGTGAGAGAGTTTGGTTAGGCAAGAGGATACCATTA 120	OY 121 TGGTCTCATTGAGAGAGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAAGTATGC 180	Oy 181 TCAAATCCAGGGTTTTTGTGGTCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCAT 240	OY 241 TCAAGCTAAGACTGGAAGATACAAAAACCCTGAAGAAAACGCCTTCTCCCAGAAAATT 300	OY 301 ACCACCATCAATGIGCCAICTTACTCCAACATTTTTGCATCCTGGTGCTGCTTC 360	OY 361 AATTAACATAAACAAGTCCATCTGGAAAATGTATTTCAAAGAGTTACTTCCATTGCTTGC	QY 421 TACTTCGGGTGATGATGACCAATGCGCAAACTGCAGCTAATGACTTTTTTGCA 480	QY 481 GTCCATCTGGAAGGATTCACTATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGC 540	OY 541 TCCTCAAGACTACGAGCCTTTAATTCGAGCTAAGGATAGAAGGATTGATT	OY 601 GACATTTACAAGCGTTGAAGACGGTGAGGAAGAGTTGAAAAGAAGCTGTGGTGTT 660	Oy 661 TGGGCAGGAAGTGAATCTTAACAGTGATGACAATGAAAAGCGTAAATTTGATCC 720	Qy 721 ATCAGTGGCTTCTAGCTTGTACAAAAATTGGGTGATACCTCTCACCAAGGAGGTTCAGGT 780		Qy 841 TGGAAGATGAATATGATGTTGTTGAAGTGATTAAGGTGTTAAGTGATCTTTATTGC 900	1
QY         181         TCAAATCCAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCAT         240           Db         181         TCAAATCCAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTAAGAATACAGAGGCCAT         240           QY         241         TCAAGCTAAGGCTGGAAGATACAAAACCCTGAAGAAAACGCTTCTTCCCAGAAAATTT         300           Db         241         TCAAGCTAAGGCTGGAAGATACAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAAATTT         300	QY 301 ACCACCATCAATTGTGCCATCTTACTCCTACAACAGTTTTTGCATCCTGGTGCTTC 360	QY 361 AATTAACATAACAAGTCCATCTGGAAAATGTATTTCAAAGAGTTACTTCCATTGCTTGC	QY 421 TACTTCGGGTGATGACGAACTATGCGCAAACTGCAGCTAATGACCTTTCATTATGCA 480 Db 421 TACTTCGGGTGATGATGACTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCA 480	OY 481 GTCCATCTCTAGAAGGATTCACTAIGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGC 540 Db 481 GTCCATCTCTAGAAGGATTCACTAIGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGC 540	QY 541 TCCTCAAGACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTT 600 Db 541 TCCTCAAGACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTT 600	OY 601 GACATTIACAAGGGTTGAAGAGACGGTGAGGAAGAGAGTTGAAAAGAAGGCTGTGGTGTT 660 	OY 661 TGGGCAGGAAGTGAATCTTAACAGTGATGACAATGACAATGAAAACCGTAAATTTGATCC 720 Db 661 TGGGCAGGAAGTGAATCTTAACAGTGATGACAATGACAATGAAAACCGTAAATTTGATCC 720	Qy 721 ATCAGTGGCTTCTAGCTTGTACAAAATTGGGTGATACCTCTCACCAAGGAGGTTCAGGT 780	Qy 781 TGAGTACCTCTTGCGCCGTCTAGACGCATTACAATGCAGTTAGAATTTAGAAGAA 840 Db 781 TGAGTACCTCTTGCGCCGTCTAGAAGGCATTACAATGCAGTTAGAATTTAGAAGAA 840	OY 841 TGGAAGATGAATATGATGTTGTTGTAAATGATTAAGCTCTTAAGTGATCCTTTATTGC 900  Db 841 TGGAAGATGAATATGATGTTGTTGAAGATTAATGATTAAGCTCTTAAGTGATCCTTTATTGC 900	Qy 901 CAACTICATGIAGCIGIIGAITCAGAAAIAITATITGIAGCIAIAGAIIGIITACCITIAI 960 	OY 961 TTTCATCGCTTTATTAGAAAAGGCATTATTATATCATGATCTTCAAAAAAAA	RESULT 2 US-10-624-061-15	; Sequence 15, Application US/10624061 ; Publication No. US20040019929A1 ; GEBREAL INFORMATION:	u, C Giar N: A		; PRIOR FILING DATE: 1999-12-03; PRIOR APPLICATION NUMBER: 60/110,845

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                                                                                                                                     668 GAAGTGAATCTTAACAGTGATGACAATGACAATGAAAACCGTAAATTTGATCCATCAGTG
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                             GACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAATTGTTGACATTT
                                                             635 GACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTTGACATTT
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Sequence 93036, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Yongwel

TITLE OF INVENTION: Soy Nucleic Acid Molecules and

TITLE OF INVENTION: Plants and Uses Thereof for P

FILE REPRENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO SEQ ID NOS: 285684
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Sequence 7639, Application US/10425114
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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Best Local Similarity 100.0%; Pred. No. 7.8e-255;
Matches 985; Conservative 0; Mismatches 0;
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ORGANISM: Glycine max
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US-10-425-114-7639
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Publication No. US2004003488A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Shous
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
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 CAGGGTTTTTGTGGCCTCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCATTCAAGGT
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US-10-425-114-15059
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                                                                                                                                                                                          GGTGGAATTTGTTGATAAGAATACAGGCCATTCAAGCTAAGGCTGGAAGATACAAAAA
                                                                                                                                                                                                                                                     CCCTGAAGAAAAGGCCTTCTTCCCAGAAAATTTACCACCATCAATTGTGCCATCTTACTC
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                                                                                                                                                              Gaps
                                                                                                                                                              4
                                                                                                                                 Length 992;
                                                                                                                                                              Indels
                                                                                                                                  13;
                                                                                                                               Score 689.4; DB 13;
Pred. No. 4e-175;
0; Mismatches 56;
                                                                           ; FEATURE:
, OTHER HPORMATION: Clone ID: LIB3050-017-E9_FLI
US-10-452-114-15059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   984 GGCATTATTATATCATGATCTTCAAAA 1010
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                                                                                                                                  67.6%;
92.6%;
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15059
LENGTH: 992.
                                                                                                                                                 Best Local Similarity 92.6
Matches 747; Conservative
                                              TYPE: DNA
ORGANISM: Glycine
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RESULT 6 US-09-454-279-5 ; Sequence 5, Application US/09454279

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68 ACGCTAGCTTCTGTGAGAGGATTTGGTTAGGCAAGAGGATACCATCATTTATGGTCTC
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                     APPLICANT: Falco. S. Carl
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APPLICANT: Falco. S. Carl
APPLICANT: Falco. S. Carl
TILE APPLICANT: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE RZFERENCE: BBL299 US NA
CURRENT APPLICATION NUMBER: US/10/624,061
FRIOR APPLICATION NUMBER: US/09/454,279
PRIOR FILING DATE: 1099-12-03
PRIOR PLING DATE: LABELER FILING DATE: PRIOR FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DA
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Best Local Similarity 95.4%; Pred. No. 6.3e-115;
Matches 499; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Glycine me FEATURE: NAME/KEY: unsure LOCATION: (432) FEATURE: NAME/KEY: unsure LOCATION: (514)
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; LOCATION: (516)
US-10-624-061-5
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Faloe, S. Carl
APPLICANT: Famedu, Omolayo O.
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER PRILICATION NUMBER: 60/110,845
EARLIER PRILICATION NUMBER: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 45.6%; Score 465.6; DB 9; Length 525; al Similarity 95.4%; Pred. No. 6.3e-115; 499; Conservative 0; Mismatches 22; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 525
TYPE: DNA
ORGANISM: Glycine max
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LOCATION: (432)
FEATURE:
NAME/KEY: unsure
LOCATION: (514)
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US-09-454-279-5
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Best Local S
Matches 499
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                                                                                                                                                                                                                                                                                                     301 TCAATTGTGCCATCTTACTCCTTCAAACAGTTTTTTGCATCCTGGTGCTGCTTCAATTAAC 360
121 ATTGAGAGGCCAAGTTCCCTAGCAATTCTCACACCTATGATGAAAAGTATGCTCAAAATC
                                                                                                                                                                                 241 AAGGCTGGAAGATACAAAAACCCTGAAGAAAACGCCTTCTTCCCAGAAAATTTACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCATTCAAGCT
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                                                CAGGGTTTTTGTGGCCTCATTGGTGGAATTTGTTGAAGAATACAGAGGCCATTCAAGCT
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US-10-267-763-3
Sequence 3, Application US/10267763
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APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Douglas
APPLICANT: Boyes, Carol
APPLICANT: Hamilton, Carol
APPLICANT: Hoffman, Neil
APPLICANT: Kloti, Andreas
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITION FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITION FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITION FOR THE
TITLE OF INVENTION: MODULATION OF CHORESMATE SYNTHASE AND CHORISMATE
TITLE OF INVENTION: MODULATION OF ACTIVITY IN PLANTS
TITLE OF INVENTION NUMBER: US/10/267,763
CURRENT APPLICATION NUMBER: 09/610,040
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOUTHARD SECURE OF WINDOWS Version 4.0
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569 AATGGTTAAGAAGAGGTGCAGAAGAAAGCAGAAACGTTTGGACAAAGAAGTAAAATTCAA
                                                                                                                                                    938 AAGAGTCTTCGAATCGGATTCGGGTTCTGGTTCCAATGTACTGAGTCTTGACTTAAT
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                                                ----CAGTGATGACAATGACAATGAAAACCGTAAATTTGATCCATCAGTGGCT
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                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/10267763 Publication No. US20030077687A1 GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-10-267-763-9
                                                                                                                                                                                                                 796 CCGTCTAGACTGAA 809
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                                                                                   APPLICANT: BOYES, CASTA
APPLICANT: BOYES, CASTA
APPLICANT: Hamilton, Carol
APPLICANT: Hamilton, Carol
APPLICANT: Hoffman, Nail
APPLICANT: Woessner, Jeffrey
APPLICANT: Woessner, Jeffrey
APPLICANT: AScenzi, Robert
TITLE OF INVENTION: MODULATION OF CHORISMATE SYNTHASE AND CHORISMATE MUTASE
TITLE OF INVENTION: MODULATION OF ACTIVITY IN PLANTS
TITLE OF INVENTION: WIMBER: 2010-10-09
FILE REFERENCE: 2035DIV1
CURRENT FPLING DATE: 2002-10-09
FRIOR APPLICATION NUMBER: 09/610,040
FRIOR APPLICATION NUMBER: 09/610,040
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32.1%; Score 327.2; DB 15; Length 1006;
Best Local Similarity 64.2%; Pred. No. 2e-77;
Matches 510; Conservative 0; Mismatches 278; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
             No. US20030077687A1
                                                                      Boyes, Douglas
Davis, Keith
Hamilton, Carol
Hoffman, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Arabidopsis
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Sequence 972, Application US/09938842A

Publication No. US20040009476A9

Publication No. US20040009476A9

Publication No. US20040009476A9

Publication No. US20040009476A9

Publication No. US20040009476A9

APPLICANT: Kreps, Joel

APPLICANT: Areps, Joel

APPLICANT: Areps, Joel

APPLICANT: STEPS. REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-06-22

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 97-2
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246 TGAATACCCGGAAGAGAATCCTTTCTTCCTTGAGAACATTCCTCACTCGGTTTTTCCTAC 305
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ORGANISM: Arabidopsis thaliana
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: ALW, TONG
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1306-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECOND OF SECO
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CIGGAAAAIGIAITIICAAAGAGIIACIIICCAIIGCIIGCIACIIICGGGIGAIGAIGGCAA 441
                                                                                                                                                                                                                                                               CTATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGCTCCTCAAGACTACGAGCCTTT 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 972, Application US/09938B42A
Patent No. US20020160378A1
GENERAL INFORMATION:
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US-09-938-842A-972
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Avalic, David K.
APPLICANT: Applicant: Avalic, David K.
APPLICANT: Con Yongwei
APPLICANT: Boukharbov, Andrey A.
APPLICANT: Buckharbov, Andrey A.
APPLICANT: Li, Ring
APPLICANT: Li, Ring
APPLICANT: Li, Ring
APPLICANT: Li, Ring
APPLICANT: NurbERION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION: NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT PAPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003.04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141578
LENGTH: 694
TYPE: DNA
ONGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 1.6e-59;
0; Mismatches 88;
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                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(694)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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Best Local Similarity 79.1%;
Matches 345; Conservative
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                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
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US-10-437-963-93956
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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                                                                       DB 11; Length 798;
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                                                   ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92290C.1
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            APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Eacodu, Omolayo O.
APPLICANT: Lee, Jian-Maconary C.
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
CURRENT PLLING DATE: 1999-12-03
CURRENT PLLING DATE: 1999-12-03
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 1231
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Pred. No. 1.5e-58;
0; Mismatches 331;
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al Similarity 58.4%;
469; Conservative
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; ORGANISM: Oryza sativa
US-09-454-279-13
INFORMATION:
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Sequence 13, Application US/09454279; Publication No. US20020184658A1

RESULT 14 US-09-454-279-13

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Search completed: September 25, 2004, 02:51:17 Job time: 557 secs
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                                                                                                                Sequence 13, Application US/10624061
; Sequence 13, Application US/10624061
; Publication No. US20040019929A1
; GENERAL INFORMATION:
    APPLICANT: Falco, S. Carl
    APPLICANT: Famodu, O'modlayo O.
    APPLICANT: Lee, Ulan-Wing O'modlayo O.
    APPLICANT: Lee, Ulan-Wing US NO.
    FILE OF INVENTION: AROWATIC AMINO ACID BIOSYNTHETIC ENZYMES
    TITLE OF INVENTION: AROWATIC AMINO ACID BIOSYNTHETIC ENZYMES
    TITLE OF INVENTION: AROWATIC AMINO ACID BIOSYNTHETIC ENZYMES
    TITLE OF INVENTION UNMBER: US/10/624,061
    CURRENT PILING DATE: 1099-12-03
    PRIOR APPLICATION NUMBER: US/09/454,279
    PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-12-03
    PRIOR FILING DATE: BRALLER FILING DATE: 1998-12-04
    NUMBER OF SEQ ID NOS: 22
    SOFTWARE: Microsoft Office 97
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    INDO 13
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801 TAGACTGAAGGCATTACAATGCA
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ORGANISM: Oryza sativa
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624 CGGTGAGGAAGAGGTTGAAAAGAAGGCTGTGGTGTTTGGGCAGGAAGTGAATCTTAACA
                                                                       839 crafingaacaradedigdaagcraadecraadarcrifiddacaddagdigdarrifagedg
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on:

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1 (bases 1 to 560)
Vodkin, L., Khanna, A., Coryell, V.,
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
Vodkin, L., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other ESTs: Al973566 corresponding to Gm-c1019-435 (5/)
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
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University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
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BPF649665
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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mRNA linear EST 24-MAY-2001 max cDNA clone Gm-r1070-5781 3',

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Result No.

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/organism="Glycine max"
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// clone="Gm-ri070-5781"
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// clone="Gm-ri070-18"
// clone="The library Gm-ri070"
// organism="Claycinc"
// clone="The library Gm-ri070"
// clone="The library Gm-ri070"
// cross selected from Chinaties from various tissues and stages of development of soybean that represent 2,639 sequences from immature octyledons, 1,770
// from immature seed coats, 3,938 from flowers, and 869
// from immature seed coats, 3,938 from flowers, and 869
// from immature seed coats, 3,938 from flowers from the different libraries was used to select singletons, or a representative of each contig which were reracked to form library Gm-ri070. The coDNs clones of the reracked Gm-ri070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the the jaboratory of Enromed by Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html.
// Reacking was performed by Genome Systems, 5t. Louis, http://www.life.uluo.edu/NoresearchProjects/Soybean/index.html
// from the for Comparative and Functional Genomics, the Gerian on the source library for each clone can also information on the source library for each clone can also the ortained by referring to the Genome Systems clone ID of the organism con the source library for each clone can also the ortained con also the corresponding is also listed under contigued the corresponding can be obtained by referring to the Genome Systems clone ID of the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also the corresponding can also listed under can also can also can also can also can also can also c
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                        Email: 1-vodkin@uiuc.edu
his clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
477-3324 or context:clones@genomesystems.com or info@genome
ystems.com web site:www.genomesystems.com
Seq primer: 5'_TTTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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/ Organism = "Lyvine max" / Mol. type="mRKN" | Ab xref="taxon:3847" | Ab xref="taxon:3847" | Ab xref="taxon:3847" | Albahost="mRKN" | Symper = "rocts of 'Supernod' plants" | Albahost="mENB = "rocts of 'Supernod' plants" | Albahost="DH108" | Albahost="DH108" | Albahost="DH108" | Albahost="DH108" | Albahost="Tock of Brook = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Tock = "Toc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4353 or contact via email: ccu@resgen.com
High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tobases 1 to 563)

Shomaker, K., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaropa, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermarophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae;
                                                                                                                                                                                                             862 TIGITCAAAIGATTAAGCICTTAAGIGAICCITTATIGCCAACTICAIGIAGCIGTGAT 921
AGACTGAAGGCATTACAATGCAGTTAGAATTTAGAAGAATGGAAGATGAATATGATGTTG 861
                                                                                                   69
                                                                                                                                                                                                                                                                                                                             9
                                                                                        68 TIGITICAAATGATTAAGCTCTTAAGTGATCCTTTATTGCCAACTTCANNNNGCTGNNNAT
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Unpublished (1999)
Context: Shoemaker Pybblic Soybean EST Project
Context: Shoemaker Pybblic Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1810
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subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcobRL Life Technologies' CDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene'. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 GGTTAGGCAAGAGGATACCATCATTTATGGTCTCATTGAGAGAGCCAAGTTCCCTAGCAA 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 ATTIGITGITAAGAATACAGAGGCCATTCAAGCTAAGGCTGGAAGATACAAAAACCCTGA 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 ATTIGITGITAAGAATACAGAGGCCATTCAAGCTAAGGCTGGAAGATACAAAAACCCTGA
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51.5%; Score 525; DB 10; Length 563;
Best Local Similarity 96.2%; Pred. No. 7.1e-108;
Matches 537; Conservative 0; Mismatches 21; Indels C
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q g 8 8 ò d BG363365 S12 bp mRNA linear EST 28-NOV-2001 sac19£08.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1051-2943 5' similar to TR:Q9S7H4 Q9S7H4 CHORISMATE MUTASE 7', mRNA sequence.
BG363365.1 GI:13252454 Glydine max (soybean) Glydine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; RESULT 3 BG363365 LOCUS DEFINITION SOURCE

ACCESSION VERSION KEYWORDS

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CE Shoemaker, I. (bases 1 to 512)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Marthi, J., Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Marthi, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Hubbic Soybean EST Project

Mushington University School of Medicine
4444 Forest Park Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estGwatson, wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 397.

I. :SIZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-2943"
/tissue_type="floral meristematic mRNA"
/lab_hosf="DH108"
/lab_hosf="DH108"
/lab_hosf="DH108"
/clone_lib="Gm-c1051"
/note="Weetor: pBluescript II SK+; Site I: ECORI; Site_2:
Xhol; The CDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
Xhol restriction site. ECORI adapters were ligated to the
blunt-ended cDNA fragments followed by Xhol digestion. The
CDNA fragments were directionally cloned into the
ECORI-Xhol restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into the
ligated cDNA fragments were transformed into the
ligated cDNA fragments were transformed into the
ligated cDNA fragments were transformed into the
ligated cDNA fragments were transformed into the
laboratory of Dr. Randy Shoemaker."
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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279 ACGCCTTCTTCCCAGAAATTTACCACCATCAATTGTGCCATCTTACTCCTTCAACAGT 338
241 ACGCCTTCTTCCCAGAAATTTACCACCATCATTGTGCCATCTTACTTCTTCTAAACAGT 300 158 61 GGCAAGAGGATACCATCATTTATGGTCTCATTGAGAGAGCCAAGTTCCCTAGCAATTCTC 120 218 240 398 TIGITAAGAATACAGAGGCCATICAAGCTAAGGCTGGAAGATACAAAAACCCTGAAGAAA 278 9 39 AACAAAGICCIGAITCIGGGAAIGIGIACACGCIAGCIICIGIGAGAGAGAITIGGIIA 99 GGCAAGAGGATACCATCTATGGTCTCATTGAGAGGCCAAGTTCCCTAGCAATTCTC ACACCTATGATAAAAGTATGCTCAAATCCAGGGTTTTTTGTGGCTCATTGGTGGAATTTG Best Local Similarity 99.8 Matches 511, Conservative Н 159 219 339 Db ò g ઠે 8 g

0

Gaps .,

50.1%; Score 511; DB 12; Length 512; 99.8%; Pred. No. 1e-104; ive 0; Mismatches 1; Indels

Query Match

301

ElectroMax DH10B host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."	Query Match 46.8%; Score 477; DB 9; Length 477; Best Local Similarity 100.0%; Pred. No. 4.7e-97; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 383 TGGAAAATGTATTTCAAAGAGTTACTTCCATTGCTTGCTACTTCGGGTGATGATGGCAAC 442	QY 443 TATGCGGAAACTGCAGCTAATGACCTTTCATTATTGCAGTCCATCTCTAGAAGGATTCAC 502	QY 503 TATGGAAAGTITGTAGCTGAGGTGAAATTCAGGGAIGCTCCTCAAGACTTACGAGCCTTTA 562	Qy 563 ATTCGAGCTAAGGATAAGAATTGATGAAATTGTTGACATTTACAAGCGTTGAAGG 622 		OY 683 ACTGATGACAATGAAAACCGTAAATTTGATCCATCAGTGGCTTCTAGCTTGTAC 742	Oy 743 AAAATTGGGTGATACCTCTCACCAAGGTTCAGGTTGAGTACCTCTTGGGCCGTCTA 802	OY 803 GACTGAAGGCATTACAATGCAGTTAGAATTTAGAAGATGGAAGATGATGT 859	RESULT 5	Z	ACCESSION BF009709 VERSION BF009709.1 GI:10709985 KEYWORDS EST.	M Glycine max (2017) (1) (1) (1) (2) (2) (2) (3) (4) (4) (4) (5) (5) (6) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  REFERENCE 1 (bases 1 to 620)  AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,	Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bwers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenaş, M.,	McCann, R., Waterston, K. and Wilson, K. TITLE Public Soybean EST Project JOURNAL Unpublished (1999) COMMENT Contact: Chamaker P Public Soybean EST Project	Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,	Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130
QY 399 AAGAGTTACTTCCATTGCTACTTCGGGTGATGATGGCAACTATGCGCAAACTGCAG 458	459 CTAATGACCTTTCATTATTGCAGTCCATCTCTAGAAGGATTCACTATGGAAAGTTTGTAG 421 CTAATGACCTTTCATTATTGCAGTCCATCTCTAGAAGGATTCACTATGGAAAGTTTGTAG 421 CTAATGACCTTTCATTATTGCAGTCCATCTCTAGAAGGATTCACTATGAAAGTTGTAG	519 CTGAGGTGAAATTCAGGATGCTCCTCAAGAC 550	*1 CIGANGIGARAIICAGGGAIGCICCICARGAC	Z	ACCESSION A1973566 1 GI:5770392  VERSION A1973566.1 GI:5770392  COURTON A1973566.1 GI:5770392	SOURCE GIYZINE MAX (SOYDEAN) ORGANISM GIYZINE MAX SPERALPOPLA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Phaseoleae;	Glycine. REFERENCE 1 (bases 1 to 477) AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,	Andria, A., Marka, Marka, M., Hiller, L., Macka, T., Markin, J., Beck, C., Wylie, T., Underwod, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,	MCCALL,K., WATETSTOR,K. AND WILSON,K. TITLE Public Soybean EST Project JONENAL Unpublished (1999) COMMENT Contact: Shoemaker R/Public Soybean EST Project	Public Soybean EST project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information	call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 653 Std Error: 0.00 Seq primer: -40RP from Gibco	FEATURES Location/Qualifiers  Source 1477  /organism="Glycine max"	/mol_type="mRNA" /db_xref="taxon:347" /clone="GRNOME SYSTEMS CLONE ID: Gm-c1019-435" /tissue type="immature seed coats of greenhouse grown	DRL)" (Life Technologies); Site	Site 2: Sal I; This cDNA library was constructed from mkNA isolated from immature seed coats (200-300 mgs) of genehouses grown plants. The library was prepared using the library was prepared using	construction kit Complementary NA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the	blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli

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EST 06-SEP-2000
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                                                                                                                                                                             Eukaryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermartophyta; Gore eudicots; Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                 I (bases 1 to 639)
Harris, N., Chapman, B.P. and Gijzen, M.
Gene expression in developing soybean seed coats
Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada NSV 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 639;
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                                                                         639 bp mRNA li
2-B12 GmaxSC Glycine max cDNA, mRNA sequence.
BE660542
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596 AAACTACGAAGCCTCTATTCGAGCT 620
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Glycine max
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BE660542
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                                                                                  South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 404.
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          from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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Pred. No. 1.1e-92;
0; Mismatches 119; Indels
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTs from roots of Medicago truncatula after Rhizobium inoculation Unpublished (1999)
Contact: VandenBosch K
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(Loases 1 to 648)

1 (Dases 1 to 648)

VandenBosch, K., Hurt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="pkV3-23M13"
/tissue type="Seedling roots"
/dev stage="3 days post-inoculation with Sinorhizobium
meliloti"
TTGTACAAAATTGGGTGATACCCTTTACCAAGGAGGTTCAGGTTGAGTACCTATTGCGG
                                                                                                                                                                        CGTCTAGACTGAAGGCATTATAATGCAGTTAGAAATTTACAAGAATGGAAGTGAATATGA
                                                                                                                                                                                                                 TGTTGTTGAAATGATTAAGCTCTTAAGTGATCCTTTATTGCCAACTTCATGTAGCTG
                                                                                                                                                                                                                                                                                                                                 481 TIGATIAAAAATATITAAATIGTAGCITIAGATIGGIACTITITATITITCATCGGCTITAT
                                                                                                                                     CGTCTAGACTGAAGGCATTACAATGCAGTTAGAATTTAGAAGAATGGAAGATGAATATGA
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University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 642 2755
Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
                                                                                                                                                                                                                                                                                                                                                                    976 T---AGGAAAAGGCATTATTATCATGATCTTCAAAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                           541 TAGAAGAAAAAAAAGGATTAGATCATGAACTTCAATA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  More information is available at...
http://chrysie.tamu.edu.du/acdicago
Seq primer: SKmod (CTA u/medicago
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
|mol_type="mRNA"
|cultivar="genotype A17"
|db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas A&M EST name:T258044e
TIGR sequence name:MTEBC79TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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VERSION
KEYWORDS
SOURCE
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COMMENT
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AW774625
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Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall,
1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1241
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW775842 654 bp mRNA linear EST 07-SEP-2000 EST334907 DSIL Medicago truncatula cDNA clone pDSIL-3E8, mRNA
                                                                                                601
                                                                                                                                                                                                                                          661
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTS from leaves of Medicago truncatula after inoculation with Collectrichum trifolii
Unpublished (2000)
                                        TTTGATCCATCAGTGGCTTCTAGCTTGTACAAAAATTGGGTGATACCTCTCACCAAGGAG
                                                                                             542 frigarccarcacracricraagricraranaangggraaraccrcrraangan
                                                                                                                                                                                                                                          602 GGTCAAGGTTGAGTACCTACTGCCCCCGGTTGGATTGAAACCATTATTATTTCAATGTAA
                                                                                                                                                                           GTTC-AGGTTGAGTACCT-CTTGCGCCGTCTAGACTGAAGGCATTACAATGCAGTTAGAA
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rrifolii"
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mol type="mRNA"
cultivar="genotype A17"
db_xref="taxon:3880"
/clone="pDSIL-3E8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minnesota sequence name:M259175e
TiGR sequence name:WTPAJ28TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT o
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                    662 TITICAAGAAGGAACATATAANAICAT 688
                                                                                                                                                                                                                                                                                                                 831 TITAGAAGAATGGAAGATGAATATGAT 857
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AW775842.1
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ORGANISM
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VERSION
KEYWORDS
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AW775842
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//tissue_rype="Developing flowers"
/dev_stage="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of very young, developing fully-opened flowers and flowers in early transition into pods."
/clone_lib="Developing flower"
/clone_lib="Developing flower"
/note="Wector: Lambda Zap, cDNA was prepared from polyA+enried, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap RR vector (Stratagene) and packaged using the Gigapack II Gold packaging extracts. Phagemids containing cDNA inserts were using extasts helper phage and the E. coli strain XII-Blue MRR' (Stratagene). Excised plasmids were plated using SOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGATGCTCCTCAAGACTACGAGCCTTTAATTCGAGCTAAAGGATAAAGAAGGATTGATG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATTGTTGACATTTACAAGCGTTGAAGAGACGGTGAGGAAGAAGAGTTGAAAAGAAGGCT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 GTGGTGTTTGGGCAGGAAGTGAATCTTAACAGTGATGACAATGACAATGAAAACCGTAAA 712
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                                 Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
                                                                                                                              Tel: 580 221 7391
Fax: 580 221 7390
Email: gdmay@noble.org
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Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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/clone="NF091B12FL"
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   Contact: May
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/clone lib="Blicited cell culture"
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cell wall extracts equivalent to Sugyma glucose in the
final concentration. Samples were taken at 0.5, 1, 2 and
24 hours after induction. Equal amounts of RNA from
each
time point were pooled and used for mRNA isolation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAGAATGAATATACTCTTGATACAGTGAGGAGACTTTGGTTAGACAAGAAGATACAA
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82.1%; Pred. No. 1.7e-83;
ive 0; Mismatches 104; Indels 0;
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  Seg primer: TCACACAGGAAACAGCTATGAC
                    Location/Qualifiers
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Matches 478, Conservative
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                                                                   54 CTGGGAATGTGTACACGCTAGCTTCTGTGAGAGAGATTTGGTTAGGCAAGAGGATACCA
                                                                                                      CAGAGAATGAATATACTCTTGATACAGTGAGGGAGACTTTGGTTAGACAAGAAGATACAA
                                                                                                                                                                                                                                            174 AGTATGCTCAAATCCAGGGTTTTTTGTGGCTCATTGGTGGAATTTGTTGTTAAGAATACAG
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  Pred. No. 9.5e-87;
); Mismatches 103; Indels
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Thant Balology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
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Insert Length: 605 Std Error:
Plate: 081 row: H column: 11
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Khama, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
McCarn, R., Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M.,
Unpublished (1999)
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-433 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 30-NOV-2001
SYSTEMS CLONE
                                                                                                                                                                                                                                                                                                                                                                                                                                    BM093460 560 bp mRNA linear EST 30-NOV-2001 saj09c02.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1065-9724 5' similar to TR:Q9S7H4 Q9S7H4 CHORISMATE MUTASE
             361 ATCCATCAGTGGCTTCTAGCTTGTACAAAATTGGGTGATACCTCTCACCAAGGAGGTTC 420
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1810
Fax: 314 286 1810
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Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mcNa" | /mol_type="mcNa" | /mol_type="mcNa" | /mol_type="mcNa" | /mol_type="mcNa" | /mol_type="germinating shoots" | /lab_host="pH108" | /mol_type="germinating shoots" | /mol_host="pH108" | /mol_type="germinating shoots" | /mol_type="mol_type" | /mol_type="molty" | /mol_type="molty" | /mol_type="molty" | /mol_type="molty" | /mol_type="molty" | /mol_type="molty" | /molty" |
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87.0%; Pred. No. 1.3e-80;
tive 0; Mismatches 0;
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BM093460
BM093460.1 GI:17022426
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 402.
Location/Qualifiers
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/note="Vector: unknown; Site 1: unknown; Ins Library is assigned to clones that are of uncertain origin due to an error during re-array, prepping, and/or analysis. Samples assigned this library are still genuine Glycine Max cDNA sequence, but we are unsure of its source and identification. Due to the clone id being incorrectly assigned, THESE CLONES ARE NOT AVAILABLE TO ONDER.
                                                                                                                                                                                                    1. (Jasses 1 to 422)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khana, A., Bolla, B., Marra, M., Hillier, E., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Materston, R. and Wilson, R., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Bmail: est@watson.wustl.edu
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/db_xref="taxon:3847"
/clone="GENOWE SYSTEMS CLONE ID: Gm-c1032-2453"
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                            /noce="Organ: Nodule; Vector: pSPORT1; Site 1: Sal1; Site_2: Not1; The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."
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/clone lib="Lotus japonicus nodule library 5 and 7 week-old"
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Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional (Unpublished (2000)
Contact: Udvardi MK
Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
                                                                                                                                                                                                                                     Query Match
39.3%; Score 400.4; DB 14; Length 529;
Best Local Similarity 85.3%; Pred. No. 8.5e-80;
Matches 446; Conservative 0; Mismatches 77; Indels 0;
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                                                                                            Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M. Lotus japonicus root nodule ESTs: tools for functional Unpublished (2000)
Contact: Udvardi MK
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Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Exa: 49 331 567 8250
Email: udvarci@mpimp-golm.mpg.de
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/organism="Lotus corniculatus var. j
/organism="Lotus corniculatus var. j
/mol type="mRNA"
/cultivar="Gifu (B-129)"
/db xref="taxon:34305"
/db xrege="5 and 7 week-old plants"
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                                                                                                                                                                                                                                                                                                                                                                                         CTGATICTGGGAATGTGTACACGCTAGCTTCTGTGAGAGAGGATTTGGTTAGGCAAGAGG 107
                                                                                                                                                                                                                                                                                                                                                                                                                     265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAAAGTATGCTCAAATCCAGGGTTTTTGTGGCTCATTGGTGGAATTTGTTGTAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 ACACTGAGGCCATTGAGGTATGGCTGGAAGGTACCAAAACCCTGAAGAAAATGCCTTCT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCAGAAAATTTACCACCATCAATTGTGCCATCTTACTCCTTCAAACAGTTTTTGCATC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTGCTGCTTCAATTAACAATAACAAGTCCATCTGGAAAATGTATTTCAAAGAGTTAC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICCATTGCTTGCTACTTCGGGTGATGATGGCAACTATGCGCAAACTGCAGCTAATGACC 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGAGCTGCTTCCATTAACATAACAAGTCGATTTGGAAAAATTACTTTGATGAGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tricarratidicadecaarcicaaaagarricarratidaaaagririgragecigageega
                                                                                                                                                                                                    /note="Organ: Nodule; Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; The library was prepared using mRNA extracted from nodules of 5 and 7 week old Lotus plan Nodules were induced by, and contained Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                               /organism="Lotus corniculatus var. japonicus"
| mol_type="mana,"
| cultivar="difu (B-12)" |
| db_xref="taxon:34305" |
| dev_stage="5 and 7 week-old plants" |
| clone lib="Lotus japonicus nodule library 5 and 7 week-old plants" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eudicots;
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0
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Glycine max
Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eu
                                                                                                                                                                                                                                                                                                                                                            82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATICAGGGAIGCICCICAAGACIACGAGCCITIAATICG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTCAGGGAATCTCCTCAAGACTATGAGCCTTTAATTCG 605
                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                        Score 388.8; DB 1
Pred. No. 3.4e-77;
0; Mismatches 82
Email: udvardi@mpimp-golm.mpg.de
Seg primer: T7
         Seq primer: 17
Seq primer: 17
High quality sequence stop: 605.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA800612
CA800612.1 GI:26057698
                                                                                                                                                                                                                                                                                                                          38.1%;
84.2%;
                                                                                                                                                                                                                                                                         strain R7A.
                                                                                                                                                                                                                                                                                                                                                       Matches 438, Conservative
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                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                          Local
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CA800612
LOCUS
DEFINITION
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SOURCE
ORGANISM
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VERSION
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/clone_libs-gm-clo62"
/note=TVector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into bHIOB host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khoema, R., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                           Mushington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Exa: 314 286 1810
Exa: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="stem tissue of greenhouse grown plants" /dev_stage="1 month old" /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAGCTAAGGCTGGAAGATACAAAAACCCTTGAAGAAAACGCCTTCTTCCCCAGAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 TGATGCACTTGCTGGAAGATACAAAAACCCTGAAGAAAACGCCTTCTTCCCCAGAAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTICGGGTGATGGCAACTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507 TACTICGGGTGATGATGGCAACTATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GICCATCICIAGAAGGATTCACIATGGAAGTTTGTAGCTGAAGTTGAAGATTCAGGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 ACCACCATCAATTGTGCCCATCTTACTCCTTCAAACAGTTTTTTGCATCCTGGTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GICCAICTCAAAAGATICACIAIGGAAAGITIGIAGCIGAGGIGAAAIICAAGGGAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTCAAGACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTT
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                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .726
/organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 409.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: -40RP from Gibco
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627 TCCTCAAGACTACGAGCCTTTAATTCGAGCTAAGGATAAAGAAGGATTGATGAAATTGTT 686

ò d D

Dp

Search completed: September 25, 2004, 01:24:49 Job time: 3099 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model protein δ

Sept,ember 25, 2004, 01:24:55 Run on:

5 ; Search time 74 Seconds (without alignments) 996.553 Million cell updates/sec

US-10-624-061-16

1339 1 MAKAAEQSPDSGNVYTLASV......NWVIPLTKEVQVEYLLRRLD 261 Title: Perfect score: Sequence:

BLOSUM62

Scoring table:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched:

1586107 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* .: geneseqp1980s:\* : geneseqp1990s:\* geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Abu08094 Soybean c	Aam49654 A. thalia	Abb93424 Herbicida	Abu08098 A. thalia	Aam49655 Construct	Abb92474 Herbicida	Abu08097 A. thalia	Abu08093 Rice chor		_		_	Arabic				Aao19566 M sterili	Aab11451 H. polymo	Abu08087 Protein e	Abu08088 Protein e		Aau35676 Haemoohil	0	3 Novel hu	9
SUMMARIES		ID	ABU08094	AAM49654	ABB93424	ABU08098	AAM49655	ABB92474	ABU08097	ABU08093	ABU08089	ABU08092	ABB91515	ABU08095	AAG06003	AAG06002	AAG06001	ABU08090	AA019566	AAB11451	ABU08087	ABU08088	ABU00704	AAU35676	ABU30650	ABG25473	AAG82076
		BB :	9	ഹ	ហ	9	'n	വ	φ	ø	Q	ø	Ŋ	9	m	ന	ო	9	9	ო	w	9	9	4	Q	4	4
		Length	261	265	265	265	m	334	334	257	132	331	316	207	319	325	347	154	263	280	93	62	360	781	781	665	459
do	Query	Match	100.0	61.1	61.1	61.1	61.1	52.1	52.0	50.9	50.3	50.1	50.0	45.0	44.8	44.8	4.	36.5	ä	31.6	11.0	9.8	7.8	7.7	7.7	7.2	7.2
		Score	1339	818	818	818	818	698		681.5	673	670.5	669.5	602	599.5	599.5	599.5	489	424.5	423	147	131	105	103	103	96.5	96
	Result	o N	1	0	m	4	Ŋ	v	7	œ	σ	10	11	12	13	14	.15	16	17		19	20	21	22	23	24	25

Aag82730 S. epider Abn39856 Stanhvloc		Abg04999 Novel hum	Abu25591 Protein e	Abb57939 Drosophil	Abr52685 Protein s	Abu58233 Rice stre	Ada20823 Rice beta	Abu25397 Protein e	Aaw69223 HAP4 prot	Abu44329 Protein e	Adc95055 E. faeciu	Adb23150 Environme	Aab41660 Human ORF	Aab97911 Human G-p	Abp69390 Human pol	1 Human	Aay29460 African h	Abu24103 Protein e
AAG82730 ABP39856				ABB57939	ABR52685	ABU58233	ADA20823			ABU44329		ADB23150		AAB97911	ABP69390	ADE14371	AAY29460	·ABU24103
459 4	594 6		~	_				676 6					'n	•	m		1072 2	9 965
2.7	7.1	7.0	7.0	ø.	6.9		6.8		8.9	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	6.5
o o	95.5	94	93.5	92.5	92	91.5	91.5	91.5	30.2	90	89.5	88.5	88.5	88.5		88.5	88	87.5
26 27	28	Ω : Ω :	0 %	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Soybean, plant, enzyme, chorismate mutase, aromatic amino acid, diet, biosynthesis, chorismate, anthranilate, tryptophan, prephenate, tyrosine, phenylalanine, prephenate dehydrogenase, herbicide, food crop. ABU08094 standard; protein; 261 AA Soybean chorismate mutase protein. (first entry) 22-MAY-2003 ABU08094; ABU08094 ID ARTO 

Glycine max.

05-DEC-2002.

US2002184658-A1.

99US-00454279. 03-DEC-1999; 98US-0110845P. 04-DEC-1998;

(FALC/) FALCO S C. (FAMO/) FAMODU O O. (LEEJ/) LEE J.

٦, Lee Falco SC, Famodu OO,

WPI; 2003-328651/31. N-PSDB; ABX93058. New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.

Claim 11; Fig 1; 32pp; English.

The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets converted to anthranilate amino acid biosynthetic pathway chorismate is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polynucleotide that affects the level of expression of a tyrosine

Preparing fine chemicals, particularly Vitamins E and K, useful as antioxidants e.g. in foods or medicine, by growing organisms with altered

9; Page 60-61; 74pp; German

Claim

antioxidants e.g. in foods or m shikimate biosynthesis pathway.

N-PSDB; ABA99613

This invention describes a novel method for the preparation of fine chemicals by culturing organisms in which the shikimate pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutase and/or containing a plastid transit peptide, a chorismate mutase and/or cortaining a plastid transit peptide, a chorismate mutase and/or cortaining a plastid transit peptide, a chorismate mutase and/or cortaining a plastid transition in plants. The method is used to produce chemicals, particularly Vitamins B or K and/or ubiquinone, useful e.g. as fat-soluble antioxidants (in feeds, pharmaceuticals and cosmetics), but also aromatic amino acids, salicylic or folic acid derivatives, companies with increased vitamin E contents have improved resistance to plants with increased vitamin E contents have improved resistance to shikimate pathway are useful as foods, fodder and in preparation of shikimate pathway are useful as foods, fodder and in preparation of processed foodbruffs: Transgenic plants with maltered content of desired chemicals, particularly tocopherols and/or tocotrienols. This sequence represents the Arabidopsis thaliana cytosolic chorismate mutase-2 protein used in the method of the invention

Sequence 265 AA

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Shikimate pathway; chorismate mutase; prephenate dehydrogenase; vitamin B; vitamin K; ubiquinone; fat-soluble antioxidant; transgenic; feed; pharmaceutical; cosmetic; aromatic amino acid; salicylic acid; folic acid; phenylpropanoid; flavanoid; plant; abiotic stress resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 IRAKDKEGLMKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPL 180
biosynthetic enzyme polypeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and oversypression of these enzymes may be used to increase the content of aromatic amino acid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used to design and/or nucleic acids may be used to create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits
                                                                                                                                                                                                                                                                                                                                                                                                   SLVEFVVKNTEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKOFLHPGAASININKSI 120
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                                                                                                                                                                                                                                                                    100.0%; Score 1339; DB 6;
100.0%; Pred. No. 2.2e-133;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-2000; 2000DE-01030647.
21-DEC-2000; 2000DE-01064454.
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                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 261; Conservative
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                                                                                                                                                                                                                                         Sequence 261 AA;
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                                             1 MAKAAEQSPDSG--NYYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEXYAQIQGF
                                                           SIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYE
                                                                                                                                                       PLIRAKDKEGLMKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKF--DPSVA
                                                                                                                                                                                                           181 PAIRAQDRBALMKLLIFEKVERMVKKRVQKKAETPGGEVKFNSGYGDESKKKYKVDPLLA
                                                                                             59 CGSLVEFVVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININK
                        Gaps
                           4
tch 61.1%; Score 818; DB 5; Length 265; al Similarity 61.1%; Pred. No. 5.3e-78; 162; Conservative 31; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Herbicidally active polypeptide SEQ ID NO 2635.
                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                Local Similarity
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      Query Match
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Lee J;

98US-0110845P.

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New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
                                                                                                                                                                                                            Example 3; Fig 1; 32pp; English.
                                                                                           Falco SC, Famodu OO,
                                  (LEEJ/) LEE J.
                                                                                                                  WPI; 2003-328651/31
                04-DEC-1998;
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                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for harbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor off 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                    Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MARVFESDSGSGCSNVLSLDLIRESLIRQEDTIVFSLIERAKFPLNSPAFEESRCLDSGS
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                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                    61.1%; Score 818; DB 5; Length 265; 61.1%; Pred. No. 5.3e-78; ive 31; Mismatches 68; Indels
                                                                                                                                                                   Claim 5; SEQ ID NO 2635; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. thaliana chorismate mutase protein #2.
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 28-AUG-2001; 2001WO-EP009892
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Matches 162; Conservative
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                                                   Weidler
                                                                            WPI; 2002-269010/31
                          (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                            Sequence 265 AA;
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                                                                                                   Identifying
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The invention discloses isolated polymucleotides encoding chorismate

mutase polypeptides. Aromatic amino acids must be included in the diets

of animals. In the aromatic amino acids must be included in the diets

of animals. In the aromatic amino acid biosynthesic and is converted

converted to anthranilate during tryptophan biosynthesis and is converted

to playnthesis. Chorismate mutase catalyses the conversion of chorismate to

prophenate. Also disclosed are methods for selecting an isolated

polymucleotide that affects the level of expression of a tyrosine

polymucleotide that affects the level of expression of a tyrosine

consume enzyme polypeptide in a host cell. Obtaining a uncleic acid

fragment encoding a tyrosine biosynthetic enzyme polypeptide and

evaluating compounds for their ability to inhibit the activity of a

tyrosine biosynthetic enzyme. The polypeptides can be used produce

controlles. Chorismate mutase and prephenate dehydrogenase are good

targets for herbicides that will not affect animals, and overexpression

con these enzymes may be used to increase the content of aromatic animo

con these enzymes may be used to increase the content of aromatic animo

con these enzymes of those enzymes that may be used as herbicides. The

identify inhibitors of those enzymes that may be used as herbicides. The

concletic acids may be used to create transgenic plants, as probes for the

concletic and physical mapping of the genes and as markers for traits

conclusing the mutase protein #2

conclusing the mutase protein #2
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llarity 61.1%; Pred. No. 5.3e-78;
Conservative 31; Mismatches 68;
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es 162; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 265 AA;
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99US-00454279

03-DEC-1999;

17-MAY-2002 (first entry)

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This invention describes a thore in which the shiking pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutase and/or prephenate dehydrogenase, linked to a least one regulatory sequence for transcription or translation in plants. The method is used to produce chemicals, particularly vitemains B or K and/or ubiquinone, useful e.g. as also aromatic amino acids, salicylic or folic acid derivatives, phenylpropanoids, flavanoids etc., especially in transgenic plants. Also plants with increased vitamin E contents have improved resistance to abiotic stress, e.g. frost and drought. Transgenic plants with an altered shikimate pathway are useful as foods, fodder and in preparation of processed foodstuffs. Transgenic plants with modified shikimate pathways have increased content of desired chemicals, particularly tocopherols and/or tocotrienols. This sequence represents the construct pCR-script/AtCM-ITP-ATCM-2 which is composed of the Arabidopsis thaliana plastid chorismate mutase-1 transit peptide and a Arabidopsis thaliana chorismate mutase-2 fragment and is used for plastid localisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing fine chemicals, particularly Vitamins E and K, useful as antioxidants e.g. in foods or medicine, by growing organisms with altered shikimate biosynthesis pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 SIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYE 178
                                                                                  Shikimate pathway; chorismate mutase; prephenate dehydrogenase; vitamin B; vitamin K; ubiquinone; fat-soluble antioxidant; transgenic; feed; pharmeceutical; cosmetic; aromatic amino acid; salicylic acid; folic acid; phenylpropanoid; flavanoid; plant; abiotic stress resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for the preparation of fine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.1%; Score 818; DB 5;
.larity 61.1%; Pred. No. 7.3e-78;
Conservative 31; Mismatches 68;
                                         Construct pCR-script/AtCM-1TP-AtCM2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sommer S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Page 64-65; 74pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUNG-) SUNGENE GMBH & CO KGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunze I,
                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2000; 2000DE-01030647.
21-DEC-2000; 2000DE-01064454.
                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001; 2001WO-EP007391.
                                                                                                                                                                        tocopherol; tocotrienol
                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geiger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-164442/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABA99614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 330 AA;
                                                                                                                                                                                                                                                                                 WO200200901-A1
                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Badur R,
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246 PAIRAQDREALMKLLIFEKVEEMVKKRVQKKAETFGGEVKFNSGYGDESKKKYKVDPLLA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 MKLLIFFISVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR------KFDPSVASSLYK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 TEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 PLIRAKDKEGLMKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKF--DPSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYBPLIRAKDKEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; SEQ ID NO 1685; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.1%; Score 698; DB 5; 50.4%; Pred. No. 4.2e-65;
                                                                                                                                                                                                                                                            Herbicidally active polypeptide SEQ ID NO 1685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Mismatches
                                                                                                                                                                                                                                                                                             Herbicidal; plant; agriculture; herbicide.
                                                                             306 SRIYGEWLIPLTKLVEVEYLLRRLD 330
                                                             261
                                                             SSLYKNWVIPLTKEVQVEYLLRRLD
                                                                                                                                                                     ABB92474 standard; protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2001; 2001WO-EP009892.
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weidler M;
                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                       MO200210210-A2.
                                                                                                                                                                                                                                 31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organisms.
                                                                                                                                                                                                   ABB92474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymelectide that affects the level of expression of a tyrosine polymelectide that affects the level of expression of a tyrosine polymelectide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce artibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of those enzymes may be used to increase the content of aromatic amino acid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used to design and/or increase in an animal cand physical mapping of the genes and as markers for traits in the decident the dense and as markers for traits
Plant, enzyme, chorismate mutase, aromatic amino acid; diet, biosynthesis, chorismate, anthranilate, tryptophan, prephenate, tyrosine, phenylalanine, prephenate dehydrogenase, herbicide, food crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. thaliana chorismate mutase protein #1
                                                                                                                                                                                                                                                                                                                           ABU08097 standard; protein; 334 AA.
                                                                                                 NWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                            315 DWIMPLTKEVQVEYLLRRLD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 1; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0110845P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chorismate mutase protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-328651/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FALC/) FALCO S C.
(FAMO/) FAMODU O O.
(LEEJ/) LEE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002184658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                       ABU08097;
                                                                                                    242
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(FAMO/)
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52.0%; Score 696; DB 6; Length 334; 50.4%; Pred. No. 6.9e-65;

Query Match Best Local Similarity

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The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acid biosynthetic pathway chorismate is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polynucleotide that affects the level of expression of a tyrosine biosynthetic enzyme polypoptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and
                 75 DESERITEGIRNSLIRQEDSIIFGLERAKYCYNADTYDPTAFDWDGFNGSLVEYWVKG 134
                                                                     70 TEALQAKAGRYKNPEENAPPPENLPPSIVPSYSFKOFLHPGAASININKSIWKMYFKELL 129
                                                                                         130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL 189
                                                                                                                                                                190 MKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR-----KFDPSVASSLYK 241
                                                                                                                                                                                                                                        255 MDMLTPPTVEDAIKKRVEMKTRTYGQEVKVGMEEKEEEEEEGNESHVYKISPILVGDLYG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice; plant; enzyme; chorismate mutase; aromatic amino acid; diet;
biosynthesis; chorismate; anthranilate; tryptophan; prephenate; tyrosine;
phenylalanine; prephenate dehydrogenase; herbicide; food crop.
10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABU08093 standard; protein; 257 AA.
                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice chorismate mutase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                          242 NWVIPLTKEVQVEYLLRRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00454279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Famodu 00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-328651/31.
N-PSDB; ABX93057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FALC/) FALCO S C. (FAMO/) FAMODU O O. (LEEJ/) LEE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002184658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU08093;
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
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evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of these enzymes may be used to increase the content of aromatic amno acid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used as herbicides. The mucleic acids may be used to create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits linked to those genes. The sequence presented is a rice chorismate mutase
                                                                                                                                                                                                                                                                                                                                                                 CDQLMHILLTYETVERAIEHRVEAKAKIFGQEVDLGAEDNGAPPMYKIRPSLVAELYSYRI 240
                                                                                                                                                                                                                                                                                                                                                                                                                              VVKNTEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYF 125
                                                                                                                                                                                                                                                                                                                                                                                                              126 KELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 KEGLMKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR-KFDPSVASSLYKNWV 244
                                                                                                                                                                                                                                                                                                     6 EQSPDSGNVYTLASVREDLVRQEDITIYGLIERAKFPSNSHTYDEXYAQIQGFCGSLVEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean, plant, enzyme, chorismate mutase; expressed sequence tag; EST; aromatic amino acid; diet; biosynthesis; chorismate; anthranilate; tryptophan; prephenate; tryocosine; phenylalanine; prephenate dehydrogense; herbicide; food crop.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by soybean chorismate mutase expressed sequence tag
                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                    ; Score 681.5; DB 6; Length 257; Pred. No. 1.6e-63; A4; Mismatches 78; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by GGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU08089 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 IPLIKEVQVEYLLRRLD 261
                                                                                                                                                                                                                       50.9%;
52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00454279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0110845P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                       Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Famodu 00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FALC/) FALCO S C.
(FAMO/) FAMODU O O.
(LEEJ/) LEE J.
                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                         Sequence 257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002184658-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Falco SC,
                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU08089;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                             protein
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ABU08089
    8888888888888888888
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The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate to prephenate. Also disclosed are methods for selecting an isolated polymptic enzyme polypeptide in a host cell, obtaining a mucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of these enzymes may be used to increase the content of aromatic and/or identify inhibitors of those enzymes that may be used to design and/or identify inhibitors of those enzymes that may be used as herbicides. The nucleic acids may be used to create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits of linked to those genes. The sequence presented is the protein encoded by a soybean chorismate mutase expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TEAIOAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSSGKYYFKELL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn, plant, enzyme, chorismate mutase, aromatic amino acid, diet,
biosynthesis, chorismate, anthranilate, tryptophan, prephenate, tyrosine,
phenylalanine, prephenate dehydrogenase, herbicide, food crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVBFVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 TEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                chorismate dismutase, proteins and
                                                                            New tyrosine biosynthetic enzyme, chorismate dismutase, proteins ar
nucleic acids, useful for facilitating design and/or identifying
inhibitors of those enzymes that may be used as herbicides and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                           Claim 11; Page 16-17; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU08092 standard; protein; 331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corn chorismate mutase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PLLATSGDDGNY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 PLLATSGDDGNY 141
                                                                                                                                               producing antibodies.
                  WPI; 2003-328651/31
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                                         N-PSDB; ABX93053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2002.
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99US-00454279.

03-DEC-1999;

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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 726; 261pp + Sequence Listing; English.
                                                                 Herbicidally active polypeptide SEQ ID NO 726
                                                                                                                Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                               28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP009892
                  (first entry)
                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG
                                                                                                                                                                                                                 WO200210210-A2
                                                                                                                                                                                                                                                                07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses isolated polymucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of animals. In the aromatic amino acid biosynthesis and is converted to anthramilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine converted to polymuchesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymuchetic arrayme polypeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and a tyrosine biosynthetic enzyme polypeptide and cavaluating compounds for their ability to inhibit the activity of a tyrosine current biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of these enzymes may be used to increase the content of aromatic amino caid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used to design and/or caid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used to design and/or nucleic and physical mapping of the genes and as markers for traits intended to those genes. The sequence presented is a corn chorismate mutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 MKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNEN-RKFDPSVASSLYKNWVIPLT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEXLHAQVGRYXSPDEHPFFSKDLPEPRLPPMQYPRVLHPIADSININKEIWKMYFDELL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKBGL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                             chorismate dismutase, proteins and
                                                                                                                                                                                                                                                                                                                       nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
H
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                                                                                                                                                                                                                                                                                                tyrosine biosynthetic enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 1; 32pp; English
                                                                                                                                                                             Lee J;
                          04-DEC-1998; 98US-0110845P
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KEVEVAYLLKRLD 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.4%
                                                                                                                                                                          Falco SC, Famodu OO,
                                                                                                                                                                                                                                                                                                                                                                         producing antibodies.
                                                                                                                                                                                                                         2003-328651/31
                                                                         FALCO S C.
FAMODU O O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 331 AA;
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                                                                                                   (FAMO/) FAMODU (LEEJ/) LEE J.
                                                                            FALC/) FALCO
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129
                                                                                                              70 TEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL
                                                                                                                                                                                                                                                                                                                PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL
                                                                                                                                                                                                                                                MKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDND-NENRKFDPSVASSLYKNWVIPLT
                                                                                           10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
                          50.0%; Score 669.5; DB 5; Length 316; 51.4%; Pred. No. 4.1e-62; Indels 1; ive 44; Mismatches 78; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU08095 standard; protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                                                 249 KEVQVEYLLRRLD 261
                                                 Best Local Similarity 51.4
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        KEVQIEYLLRRLD
                                             Similarity
Sequence 316 AA;
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ID ABU0
XX
AC ABU0
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ABB91515 standard; protein; 316 AA.

RESULT 11 ABB91515 ID ABB9 XX AC ABB9

ABB91515

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22-MAY-2003 (first entry)

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Claim 11; Fig 1; 32pp; English.
                                                                                                  Lee J;
                                                              99US-00454279
                                                                       98US-0110845P.
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.8<sup>†</sup>
Matches 118; Conservative
                                                                                                 Falco SC, Famodu OO,
                                                                                                           WPI; 2003-328651/31.
                                                                                (FALC/) FALCO S C. (FAMO/) FAMODU O O.
                                   Triticum aestivum.
                                                                                                               N-PSDB; ABX93059.
                                             US2002184658-A1.
                                                                                                                                                                                                                                                         Sequence 207 AA;
                                                                                         (LEEJ/) LEE J.
                                                                                                                                                                                                                                                mutase protein
                                                              03-DEC-1999;
                                                                       04-DEC-1998;
                                                     05-DEC-2002.
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99US-0138847P.
99US-0139119P.
99US-0139452P.
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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16-APR-1999;
19-APR-1999;
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14-MAY-1999;
14-MAY-1999;
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27-MAY-1999;
28-MAY-1999;
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05-MAY-1999;
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18-MAY-1999;
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16-JUN-1999
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                                                                                                                                                       AAG06003;
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                                                                               RESULT 13
                                                                                               AAG060
                                                                                                                                     The invention discloses isolated polymucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymolectide that affects the level of expression of a tyrosine polymolectide that affects the level of expression of a tyrosine polymolectide in a host cell, obtaining a mucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide in a host cell, obtaining a mucleic acid evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme prephenate dehydrogenase are good tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good tragets for herbicides that will not affect animals, and overexpression of these enzymes may be used to increase the content of aromatic animo acid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used to design and/or increase and as markers for the genetic and physical mapping of the genes and as markers for traits in the account of acids may be used to create transgenic plants, as probes for the genes and as markers for traits
                                   Wheat; plant; enzyme; chorismate mutase; aromatic amino acid; diet; biosynthesis; chorismate; anthranilate; tryptophan; prephenate; tyrosine; phenylalanine; prephenate dehydrogenase; herbicide; food crop.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDKEGLMKLLTFTSVEETVRKRVEKKAVVFGGEVNL----NSDDND--NENRKFDPSVAS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 EFVVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
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Wheat chorismate mutase protein.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 2617.
238 SLYKNWVIPLTKEVQVEYLLRRLD 261
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                 184 KLYDMWVMPLTKDVEVEYLLRRLD
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10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN
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Pred. No. 1.2e-54;
5; Mismatches 71; Indels
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TEAIQAKAGRYKOPEBNAFPPENLPPSIVPSXSFKQFLHPGAASININKSIWKOMYFKELL 129

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                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                         190 MKLLTFTSVAETVRKRVEKKAVVFGQBVNLNSDDNDNANRKFDPSVASSLYK 241
                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 2616.
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                                                                                                                     130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYBPLJRAKDKEGL
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                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 2615.
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Matches 113; Conserv
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Page 13

	3; Gaps
10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN	SLVEFVVKN 69
WSLIRQEDSIIFGLLERAKYCYNADTYDPTAFDMDGFNG	LVEYMVKG 1
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130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEFLIRAKDKEGL 189	RAKDKEGL 1
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190 MKLITFTSVEETVRKRVEKKAVVFGQEVNLNSDNDNENRKFDPSVASSLYK 241	( 241
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GenCore version 5.1.6
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US-09-107-532A-4682

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Listing first 45 summaries
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Sequence 16, Application US/09454279;
Patent No. 6627798

GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian-Ming
TILIE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BL299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER PILING-DATE: 1998-12-04
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
LENGTH: 261
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US-09-071-035-334

US-09-134-0123-1

US-09-134-0123-1

US-09-224-026-28

PCT-US94-01902-28

US-09-44-184-48

US-08-318-579A-29

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US-09-561-818A-112

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US-08-232-540-1

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    TYPE: PRT
CORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 QIWDIYFKELLPLFVKPGDDGNYPSTAASDLACLQALSRRIHYGKFVAEVKFRDAPQDYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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APPLICANT: Falco, S. Carl

APPLICANT: Famedu, Cmolayo O.

APPLICANT: Famedu, Cmolayo O.

APPLICANT: Lee, Jian-Ming

TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES

TITLE REPERENCE: BB1299 US NA

CURRENT APPLICATION NUMBER: US/09/454,279

CURRENT FILING DATE: 1999-12-03

EARLIER APPLICATION NUMBER: 60/110,845

FARIER PILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

SEQ ID NOS: 22
                                   APPLICANT: Falco, S. Carl
APPLICANT: Fancdu, Cmolayo O.
APPLICANT: Famcdu, Cmolayo O.
APPLICANT: Lee, Jian-Ming
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
BARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 265;
                                                                                                                                                                                                                                                                                                                                                        Score 818; DB 4; Length 26
Pred. No. 1e-80;
1; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Lindels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
52.0%; Score 696; DB 4;
Best Local Similarity 50.4%; Pred. No. 2.8e-67;
Matches 131; Conservative 46; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLYKNWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09454279
Patent No. 6627798
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.1%; Pre
Matches 162; Conservative 31;
                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Arabidopsis thaliana US-09-454-279-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Arabidopsis thaliana
US-09-454-279-21
Patent No. 6627798
GENERAL INFORMATION:
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10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN 69

Gaps

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70 TEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL 129
                                 190 MKLLIFISVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR-----KFDPSVASSLYK 241
                                                                                                                                                                                                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DELLPRLVKEGSDGNYGSSALCDTICLQALSKRIHYGKFVAEAKFQESPEAYMPAIIAQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 KEGLMKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR-KFDPSVASSLYKNWV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                  130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 VVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 257,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Fandu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION FAROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REPERENCE: BB1299 US NA
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.9%; Score 681.5; DB 4;
52.1%; Pred. No. 7e-66;
ive 44; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-454-279-14
; Sequence 14, Application US/09454279
; Patent No. 6627798
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              242 NWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                               315 DWIMPLTKEVQVEYLLRRLD 334
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Patent No. 6627798
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famcdu, Omclayo O.
APPLICANT: Lee, Jian-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPLTKEVOVAYLLRRLD 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 IPLIKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Office 97
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Best Local Similarity 52.1%
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 YFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 EFVVKNTBALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKM
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APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, Omolayo O.
APPLICANT: Pancou, Omolayo O.
APPLICANT: Lee, Ulan-Ming
ITILE OF INVENTION: AROWATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REPREBENCE: BBL299 US NA
CURRENT APPLICATION NUMBER: 0S/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
HARLER PLING DATE: 1999-12-04
NUMBER OF SEQ ID NAS: 22
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                             APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian-Ming
FILE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REPERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,7845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.0%; Score 602; DB 4;
Best Local Similarity 57.8%; Pred. No. 2.2e-57;
Matches 118; Conservative 27; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 KLYDMWVMPLTKDVEVEYLLRRLD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 SLYKNWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                                            Sequence 18; Application US/09454279
Patent No. 6627798
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-454-279-8
; Sequence 8, Application US/09454279
; Patent No. 6627798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SOFTWARE: Microsoft Office 97; SEQ ID NO 18
. LENGTH: 207
.; TYPE: PRT
. ORGANISM: Triticum aestivum
US-09-454-279-18
                                                    319 KEVEVAYLLKRLD 331
              249 KEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                                              10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL 189
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Sequence 12, Application US/09454279;
Patent No. 6627799
Sequence 12, Application US/09454279;
Sequence 12, Application US/09454279;
Septiment No. 6627799
Sequence 12, Application Sequence 12, Applicant: Famodu, Omclayo O. Septiment Lee, Jian-Ming
TITLE OF INVENTION: APPLICANTC AMINO ACID BIOSYNTHETIC ENZYMES FILE REFERENCE: BAIL AND APPLICANTE. BEPLICATION NUMBER: US/09/454,279;
CURRENT APPLICATION NUMBER: US/09/454,279;
CURRENT PILING DATE: 1999-12-04;
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97;
SEQ ID NO 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 331;
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES FILE REFERENCE: BB1299 US NA CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ'ID NOS: 22
SOFWARE: Microsoft Office 97
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                         Length 132;
                                                                                                                                                                                                                                                                                                                                    Score 673; DB 4; Length 13
Pred. No. 2.1e-65;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                    50.3%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PLLATSGDDGNY 132
                                                                                                                                                                                                                                                                                                                                  Query Match 50.3
Best Local Similarity 98.5
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 PLLATSGDDGNY 141
                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Glycine max
US-09-454-279-6
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US-09-454-279-12
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US-09-454-279-12
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59; Conservative
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NAME/KEY: UNSURE
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61 MV 62
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US-09-134-001C-4701
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                  LOCATION: (3
US-09-454-279-4
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                                                                                                                   124 YFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRA 183
                      EFVVKNTEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 DRSDILTLDSIRQVLIRLEDSIIFGLERAQFCYNADTYDSNAFHMDGFGGSWLNIVREL 84
                                          Gaps
                                                                                                                                                                                                                                      RESULT 9

US-09-454-279-2

US-09-454-279-2

Sequence 2, Application US/09454279

Patent No. 6627798

GENERAL INFORMATION:

APPLICANT: Fanco, S. Carl

APPLICANT: Lee, Jian-Ming

TILLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES

FILE REFERENCE: BB129 US NA

CURRENT FILING DATE: 1999-12-03

EARLIER APPLICATION NUMBER: 60/110,845

EARLIER APPLICATION NUMBER: 60/110,845

SOFTWARE: Milling DATE: 1999-12-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Sequence 4, Application US/09454279 |
| Sequence 10. 6627798 |
| Patent No. 6627798 |
| GENERAL INFORMATION: |
| APPLICANT: Falco, S. Carl |
| APPLICANT: Falco, S. Carl |
| APPLICANT: Falco, S. Carl |
| APPLICANT: Lee, Jian-Ming |
| TITLE OF INVENTION: ARCMATIC AMINO ACID BIOSYNTHETIC ENZYMES |
| TITLE OF INVENTION: ARCMATIC AMINO ACID BIOSYNTHETIC ENZYMES |
| TITLE OF INVENTION: ARCMATIC AMINO ACID BIOSYNTHETIC ENZYMES |
| TITLE OF INVENTION: ARCMATIC AMINO ACID BIOSYNTHETIC ENZYMES |
| TITLE PREPRIED ENTO: 1999 US NA |
| CURRENT APPLICATION NUMBER: 60/110,845 |
| BARLIER FILING DATE: 1998-12-04 |
| NUMBER OF SEQ ID NOS: 22 |
| SOFTWARE: MICROSOFT Office 97 |
| SEQ ID NO 44 |
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11.0%; Score 147; DB 4; Length 93
Best Local Similarity 43.5%; Pred. No. 2.1e-08;
Matches 30; Conservative 15; Mismatches 24; Indels
                                                                                                                                                                          184 KDKEGLMKLLTFTSVEETVRKRVEKKAVVFGQEV 217
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 TEALQAKAG 78
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US-09-454-279-4
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US-09-543-681A-5022

Sequence 5022, Application US/09543681A

Sequence 5022, Application US/09543681A

Sequence 5022, Application US/09543681A

Setting NO. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: VOICLEIC ACID AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILL)
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILIMG DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: S674
SEQ ID NO 4701
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                                                                                                                               1 MAKAAEQSPDSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCG
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                                                Gaps
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21.1%; Pred. No. 0.094;
     Length 62;
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Query Match

9.8%; Score 131; DB 4;
Best Local Similarity 41.9%; Pred. No. 6.1e-07;
Matches 26; Conservative 14; Mismatches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Staphylococcus epidermidis
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OPERATING SYSTEM: DOS
SOFTWARE: WORD PETERS (1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,774
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,579
                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
TELEPHONE: 650-845-4166
TELERAX: 650-845-0166
TELERAX: 650-845-0166
TELERAX: 650-845-0166
TELERATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acids
TYPE: amino acids
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IBM Compatible
                    REFERENCE/DOCKET NUMBER:
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Best Local Similarity
Matches 56; Conserva
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US-09-388-774-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 575 LSQNTNLVPQYTIKNIIHENSAN-NINEDNLKKYYKDIFKLA------EIG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 LLOSISRRIHYGKFVAEVKFRDAP-----QDY--EPLIRAKDXEGL------ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 SIDAI------KFIITKEYKDKSAGDEIYQDYSFDKLTNITIKERLAWRKKCADLGNFI 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 -MKLLT--FTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLYKNWVIP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09074579

Patent No. 6001596

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
TITLE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR
NUMBER OF SEQUENCES: 5
CORRESPONDED ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                               Query Match 7.2%; Score 96; DB 4 Best Local Similarity 19.0%; Pred. No. 0.2; Matches 60; Conservative 60; Mismatches
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: WORD PEFFECT 6.1/MS-DOS
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/074,579
FILING DATE: HEREWITH
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEC ID NOS: 8344
LENGTH: 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 722 -- KEKRDNTLDYLLNQ 735
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ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5022
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US-09-074-579-3
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79 RYKNPEENAFFENLPPSIVPSYSFKOFLHPGAASININKSIWKMYFKELLPLLATSGDD 138 299 ------FAPDNLDP--IP----KNILF----VIDVSGSMWGVKWKQTVEAMKTILDD 339 340 LRAEDHFSVIDFNQNIRTWRNDLFQLQ--KHRLQIAKRYIEKIQPSGGTNINEALLRAIF 397 139 ------GNYAQTAANDLSLLQSISRRIHYGK-FVAEVKFRDAPQDYEPLIRA-- 183 184 ------KDKEGLMKLLIFTSVEETVRKRVEKKAVVFGQEVNLNS 221 398 ILNBANNLGLLDPNSVSLIILVSDGDPTVGELKLSKIQKNVKENIQDNISLFSLGMGFDV 457 19 SVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKNTEAIQAKAG 78 6.9%; Score 92; DB 3; Length 946; 19.2%; Pred. No. 0.78; tive 43; Mismatches 89; Indels 104; 222 DDN-----DNENRKFDPSVASSLYKKW-------VIPLTKEVQVEY 263 SCRETAVDGELUVLYD-VKR-----EEKAGELEVFNGYFVHF--Sequence 3, Application US/09388774

Patent No. 6228991

GARBALI INFORMATION:
GARBALI INFORMATION:
GARBALI INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
ITILE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
ITILE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STATE: CA

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Search completed: & Job time : 24 secs
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US-09-319-989-6
; Sequence 6, Application US/09319989
; Patent No. 61991014;
; Batent No. 61991014;
; GENERAL INFORMATION:
; APPLICANT: Grivell, Leslie A.
; APPLICANT: Grivell, Leslie A.
; APPLICANT: Grivell, Leslie A.
; APPLICANT: Grivell, Leslie A.
; APPLICANT: Grivell, Leslie A.
; APPLICANT: Grivell, Leslie A.
; TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF
; TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF
; TITLE OF INVENTION: METHODS FOR MOUNTERS AND MICRO-ORGANISMS OBTAINABLE BY SAID
; TITLE OF INVENTION: METHODS FOR MOUNTERS: 1870/9319,989
; CURRENT FILING DATE: 1999-06-14
; EARLIER FILING DATE: 1999-12-12
; EARLIER FILING DATE: 1999-12-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 6
; LENGTH: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 LRAEDHFSVIDFNQNIRTWRNDLFQLQ--KHRLQIAKRYIEKIQPSGGTNINEALLRAIF 397
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                                                                                                                                                                                                                                                                                                                                                                                                                     19 SVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVBFVVKNTEALQAKAG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 ILNEANNLGLLDPNSVSLIILVSDGDPTVGELKLSKIQKNVKENIQDNISLFSLGMGFDV
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                                                                                                                                                                                                                                                                                                                                                                                 89; Indels 104; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 90.5; DB 3; Length 554;
22.2%; Pred. No. 0.49;
tive 37; Mismatches 85; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: HAP4
US-09-319-989-6
                                                                                                                                                                                                                                                                                                                                           DB 3; Length 946;
                                                                                                                                                                                                                                                                                                                                             ; Score 92; DB 3; Pred. No. 0.78; 43; Mismatches
REGISTRATION NUMBER: 39,132
REFERRNCE/DOCKTAT NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                           Query Match 6.9%;
Best Local Similarity 19.2%;
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Best Local Similarity 22.23
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      56; Conservative
                                                                                                                                                                                                                       TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENEBANK

; CLONE: g133985

US-09-388-774-3
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September 25, 2004, 02:54:21; Search time 73 Seconds (without alignments) 1149.683 Million cell updates/sec
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1 MAKAARQSPDSGNVYTLASV......NWVIPLTKEVQVEYLLRRLD 261
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/RCT NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/RCT NEW PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1349238 seqs, 321558718 residues
                                                                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 16, Appl	Segmence 16, Appl	Sequence 48703. A	Sequence 235878.	Sequence 43606. A	Sequence 22. Appl	Sequence 22, Appl	Sequence 21. Appl	Sequence 21, Appl	Sequence 196439.	Secuence 14. Appl	Sequence 14. Appl	Sequence 151855.	Semence 6. Appli	Sequence 6, Appli	
SUMMARIES	US-09-454-279-16	US-10-624-061-16	US-10-425-114-48703	US-10-424-599-235878	US-10~425-114-43606	US-09-454-279-22	US-10-624-061-22	US-09-454-279-21	US-10-624-061-21	US-10-437-963-196439	US-09-454-279-14	US-10-624-061-14	US-10-437-963-151855	US-09-454-279-6	US-10-624-061-6	
	. 6	15	12	12	12	σ	15	σ	15	16	σ,	15	16	o,	15	
% Query Match Length DB	261	261	297	261	199	265	265	334	334	313	257	257	255	132	132	
% Query Match	100.0	100.0	100.0	98.2	72.4	61.1	61.1	52.0	52.0	51.2	50.9	50.9	50.7	50.3	50.3	
Score	1339	1339	1339	1315	970	818	818	969	969	685.5	681.5	681.5	678.5	673	673	
Result No.	Н	7	m	4	ស	9	7	80	σ	10	11	12	13	14	15	

Segmence 66528. A	Sequence 12, Appl	Sequence 12, Appl	e 45	Sequence 68586, A	equei	edne	Sequence 18, Appl	Sequence 18, Appl	equei	Sequence 186040,	_	_	ш	Sequence 8, Appli	Sequence 8, Appli	Sequence 224668,	Sequence 2, Appli	Seguence 38176. A	Sequence 52545, A	Sequence 272410,	Sequence 2, Appli	Sequence 2, Appli		Sequence 4, Appli	o	a	_	e 58574,	e 179
US-10-425-114-66528		US-10-624-061-1	US-10-767-701-45	US-10-425-114-6858	US-10-424-599-2666	US-10-425-114-	27	US-10-624-061-1	US-10-767-70	US-10-437-963-1	US-10-437-963	US-10-437-96	US-10-425-114-526	US-09-454-279-8	US-10-624-061-	US-10-424-599-2	US-10-04;	US-10-425-114-3	US-10-425-114-52	US-10-42	19-454-279-	US-10-624-	US-10-424-599	US-09-454-279-4	US-10-624-061-	US-10-424-599	-815-242-1126	S-10-282-122A-	
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 Sequence 16, Application US/09454279 SUS-09-444-279-16 Sequence 16, Application US/09454279 Publication No. US20020184658A1 GENERAL INFORMATION: APPLICANT: Fanciou, Omolayo O. APPLICANT: Remodu, Omolayo O. APPLICANT: Lee, Jian-Ming TILLE OF THE REPRENCE: BB1299 US NA CURRENT APPLICATION NUMBER: US/09/454,279 CURRENT PLING DATE: 1999-12-03 EARLIER PILING DATE: 1999-12-04 NUMBER OF SEQ ID NOS: 22 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Microsoft Office 97 SEQ ID NO 16 LEAVIER PILING TYPE: PT	Query Match 100.0%; Score 1339; DB 9; Length 261; Best Local Similarity 100.0%; Pred. No. 1.2e-125; Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	29 1 MAKAAEQSPDSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCG 60	SLVEFVYRNTEALQAKAGRYKNPEENAPFPENLPPSIVPSYSFKQFLHPGAASININKSI 120 	121 WKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPL
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RESULT 4
US-10-424-599-235878
US-10-424-599-235878
Publication No. US20040031072A1
Sequence 235879, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER: OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 WKWYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPL
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Best Local Similarity 100.0%; Pred. No. 1.5e-125;
Matches 261; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
98.2%; Score 1315; DB 12;
Best Local Similarity 97.7%; Pred. No. 3.1e-123;
Matches 255; Conservative 6; Mismatches 0;
                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 700677130_FLI.pep
US-10-425-114-48703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KNWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 KNWVIPLTKEVQVEYLLRRLD 297
CURRENT FILING DATE: 2003-04-28 WINDER OF SEQ ID NOS: 73128 SEQ ID NO 48703 LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
                                                                                             TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-235878
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LENGTH: 261
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US-10-425-114-48703

Sequence 48703, Application US/10425114

Sequence 48703, Application US/10425114

Sequence 48703, Application US/10425114

Sequence 48703, Application US/10405114

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114
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         9
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US-10-624-061-16

US-10-624-061-16

Sequence 16, Application US/10624061

PUBLICATION NO. US20040019929A1

GENERAL INFORMATION:

APPLICANT: Fancou, Omclayo O. APPLICANT: Fancou, Omclayo O. APPLICANT: Fancou, Omclayo O. APPLICANT: Lee, Jian-Ming

TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES

FILE REPRENCE: BB1299 US NA

CURRENT APPLICATION NUMBER: US/10/624,061

CURRENT FILING DATE: 2003-07-21

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: MICROSOFT Office 97
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Best Local Similarity 100.0%; Pred. No. 1.2e-125;
Matches 261; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KNWVIPLTKEVQVEYLLRRLD 261
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                                                                                                         241 KNWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                241 KAWVIPLTKEVQVEYLLRKLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Glycine max US-10-624-061-16
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59 CGSLVEFVVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININK 118
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                                                                                                                                                                                                                                                                                                                               119 SIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYE 178
                                                                                                                                                                                                                                                                                                                                                                                                              179 PLIRAKDKEGLMKLLIFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKF--DPSVA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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Sequence 22, Application US/10624061

Publication No. US20040019929A1

GENERAL INFORMATION:

APPLICANT: Falco, S. Carl

APPLICANT: Famodu, Omolayo O.

APPLICANT: Famodu, Omolayo O.

PILLE NEFERENCE: BB1299 US NA

CURRENT APPLICATION NUMBER: US/10/624,061

PRIOR APPLICATION NUMBER: US/09/454,279

PRIOR APPLICATION NUMBER: US/09/454,279

PRIOR PILLING DATE: 1999-12-03.

PRIOR PILLING DATE: BARLIER FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Microsoft Office 97

LENGTH . 266
                                                                                             Length 265;
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                                                                                                                                    68; Indels
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llarity 61.1%; Pred. No. 2.1e-73;
Conservative 31; Mismatches 68;
                                                                                         Score 818; DB 9;
Pred. No. 2.1e-73;
                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 SSLYKNWVIPLTKEVQVEYLLRRLD 261
          ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-454-279-22
                                                                                         Query Match . 61.1%;
Best Local Similarity 61.1%;
Matches 162; Conservative 3
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                                                                                     Query Match
Best Local Similarity
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162; Conserv
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Best Local S:
Matches 162
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APPLICANT: Schou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Green, Steven E
APPLICANT: Go, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICANTON NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
IRAKDKEGLMKLIJFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLY 240
                         VEFVVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWK 122
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Publication No. US20020184658A1
| Publication No. US20020184658A1
| Publication No. US20020184658A1
| Publication No. US20020184658A1
| APPLICANT: Falco, S. Carl
| APPLICANT: Famodu, Omolayo O. | APPLICANT: Lee, Jian-Ming
| TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
| FILE REFERENCE: BB1299 US NA | CURRENT APPLICATION NUMBER: US/09/454,279 | CURRENT FILING DATE: 1999-12-04 | CURRENT FILING DATE: 1998-12-04 | NUMBER OF SEQ ID NOS: 22 | SOFWWARE: Microsoft Office 97 | SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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US-10-425-114-43606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.4%; Score 970; DB 12; 94.0%; Pred. No. 8.2e-89; ive 8; Mismatches 4;
                                                                                                                                                                                                                   ; Sequence 43606, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                 261
                                                                                                                241 KNWVIPLTKEVQVEYLLRRLD 261
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                                                                            KNWVIPLTKEVQVEYLLRRLD
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Best Local Similarity 94.0
Matches 187; Conservative
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US-09-454-279-22
181
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130 PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL 189
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APPLICANT: Falco, S. Carl
APPLICANT: Fancolu, Omclayo O.
APPLICANT: Lee, Jian-Wing
TITLE OF INVENTION: AROWATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1299 US NA
CURRENT PELLORION NUMBER: US/10/624,061
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: BALLIER PELICATION NUMBER: 60/110,845
PRIOR FILING DATE: EABLIER FILING DATE: 1998-12-04
NUMBER OF SEO ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
LENGTH: 334
                                                                                                                                                US-01-19

Sequence 21, Application US/09454279;

Publication No. US20020184658A1

; Bublication No. US20020184658A1

; GENERAL INFORMATION:

APPLICANT: Falco, S. Carl

APPLICANT: Famodu, Omodayo O.

; APPLICANT: Lee, Jian-Ming

; TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES

; FILE REFRENCE: BBL299 US NA

; CURRENT PPLICATION NUMBER: US/09/454,279

CURRENT FILIGATION NUMBER: 60/110,845

; EARLIER APPLICATION NUMBER: 60/110,845

; EARLIER PILING DATE: 1999-12-04

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.0%; Score 696; DB 9; Length 334; Best Local Similarity 50.4%; Pred. No. 5.1e-61; Matches 131; Conservative 46; Mismatches 75; Indels
237 SSLYKNWVIPLTKEVQVEYLLRRLD 261
                                                  241 SRIYGEWLIPLTKLVEVEYLLRRLD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 21, Application US/10624061
; Publication No. US20040019929A1
; GENERAL INFORMATION:
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US-09-454-279-21
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LENGTH: 334
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APPLICANT: Wu, wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Backbarov, Andrey A.
APPLICANT: Backbarov, Andrey A.
APPLICANT: Backbarov, Andrey A.
APPLICANT: Li, Ping
ITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT PALICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 196439
                                                                                                                                                                                                                                                                                                      255 MDMLTFPTVEDAIKKRVEMKTRTYGQEVKVGMEEKEEBEBEGNESHVYKISPILVGDLYG 314
                                                                                                                                                                                                        70 TEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                         195 PRLVKKGDDGNYGSTAVCDAICLQCLSKRIHYGKFVAEAKFQASPEAYESAIKAQDKDRL 254
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                                                                                                                           8; Gaps
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                                                                          Length 334;
                                                                                                                           75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Clone ID: PAT_MRT4530_92290C.1.pep
US-10-437-963-196439
                                                                          h Score 696; DB 15; Similarity 50.4%; Pred. No. 5.1e-61; 31; Conservative 46; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 196439, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 NWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 DWIMPLTKEVOVEYLLRRLD 334
; ORGANISM: Arabidopsis thaliana
US-10-624-061-21
                                                                                                                             Matches 131; Conservative
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ORGANISM: Oryza sativa
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                                                                             Query Match
Best Local
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION: NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 KEGLMKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR-KFDPSVASSLYKNWV 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||| | |||| : | | || || || || || || ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || |
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                                                                                                                                                                                                    Length 257;
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                                                                                                                                                                                                    50.9%; Score 681.5; DB 15; Length
52.1%; Pred. No. 1e-59;
ive 44; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Indels
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US-10-437-963-151855
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; Pred. No. 2e-59;
43; Mismatches 63; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-437-963-151855
Sequence 151855, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 IPLIKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 MPĽTKEVOVAYLLRRLD 257
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Best Local Similarity 53.1%;
Matches 135; Conservative 4:
                                                                                                                                                                                                                                   Best Local Similarity 52.1
Matches 134; Conservative
   ; SEQ ID NO 14
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-624-061-14
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ORGANISM: Oryza sativa
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LENGTH: 255
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 KEGLMKLLIFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR-KFDPSVASSLYKNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYBPLIRAKD
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Publication No. US20040019929A1

GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION ARGMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/10/624,061
CURRENT APPLICATION NUMBER: US/09/454,279
PRIOR APPLICATION NUMBER: US/09/454,279
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 60/110,845
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
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Fublication No. US20020184558A1
Fublication No. US20020184558A1
Fublication No. US20020184558A1
Fublication No. US2002018458A1
Fublicant: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
APPLICANT: Lee, Jian-Mino O.
FILE REPRENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
FARLIER APPLICATION NUMBER: 60/110,845
FARLIER APPLICATION NUMBER: 60/110,845
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
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                                                                                                                                             240 YKMWVIPLTKEVQVEYLLRRLD 261
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Best Local Similarity 52.1'
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                              RESULT 11
US-09-454-279-14
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US-10-624-061-14
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LENGTH: 257
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---KFDPSVASSLYKNWVIPL 247
                          09
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APPLICANT: Falco. S. Carl
APPLICANT: Fanceu, Omolayo O.
APPLICANT: Fanceu, Omolayo O.
FILE REPERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/10/624,061
CURRENT APPLICATION NUMBER: US/10/624,061
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US/09/454,279
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/110,845
PRIOR APPLICATION NUMBER: BARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
                                                                                                                                                                                                                                     NS-09-454-279-6

| Sequence 6, Application US/09454279 |
| Sequence 6, Application US/09454279 |
| Publication No. US20020184658A1 |
| Publicant No. US20020184658A1 |
| APPLICANT: Falco, S. Carl |
| APPLICANT: Falco, Gmolayo O. APPLICANT: Lemodu, Omolayo O. APPLICANT: Lemodu, Omolayo O. APPLICANT: Lemodu, AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES |
| PILE REPERBNCE: BB1299 US NA |
| CURRENT APPLICATION NUMBER: US/09/454,279 |
| CURRENT FILING DATE: 1999-12-03 |
| BARLIER APPLICATION NUMBER: 60/110,845 |
| HUMBER OF SEQ ID NOS: 22 |
| SOFTWARE: Microsoft Office 97 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.3%; Score 673; DB 9; Length 132; 98.5%; Pred. No. 2.7e-59; Pred. O; Mismatches 2; Indels
  194 TFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10624061 Publication No. US20040019929A1 GENERAL INFORMATION:
                                                                                                248 TKEVQVEYLLRRLD 261
                                                                                                                                          242 TKDVEVEYLLRRLD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLLATSGDDGNY 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.5
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Glycine max
US-09-454-279-6
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ORGANISM: Glycine max
US-10-624-061-6
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LENGTH: 13
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                                                                                                                                                                               61 TEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSSGKMYFKELL 120
                                                                            10 DSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN 69
                                                                                                                   1 DSGNYYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKN 60
                                        Gaps
                                        ;
Length 132;
                                        2; Indels
  50.3%; Score 673; DB 15; 98.5%; Pred. No. 2.7e-59; iive 0; Mismatches 2;
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    Query Match
Best Local Similarity 98.5
Matches 130; Conservative
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September 25, 2004, 02:42:06; Search time 24 Seconds (without alignments) 1046.083 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-10-624-061-16 1339 1 MAKAAEQSPDSGNVYTLASV......NWVIPLTKEVQVEYLLRRLD 261 283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78: \*
1: pir1: \*
2: pir2: \*
3: pir3: \*
4: pir4: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	chorismate mutase	chorismate mutase	chorismate mutase		o)	chorismate mutase	hypothetical prote	ribonucleoside-dip	hypothetical prote	probable membrane	probable membrane	cal			endopeptidase La (	thiamin biosynthes	probable heat shoc	regulatory protein	inter-alpha-trypsi	DNA topoisomerase		hypothetical prote	14	DNA topoisomerase	hypothetical prote	probable homeodoma	RNA polymerase bet	KIAA1424 protein [	hypothetical prote
SUMMARIES	QH	T50796	S38958	A45921	T37784	T14902	T14901	G95041	B64135	F90044	859393	S56296	D75014	A71683	S64410	AF3361	AF0932	H81414	837936	JC5575	JC6552	B70163	C84568	H70302	G90241	**	8477	046	A59438	0
	DB	!			N																							N	N	73
	Length	265	334	256	251	82	70	360	781	587	1556	295	1134	371	605	823	631	439	554	946	1015	251	1187	431	668	578	680	1468	94	484
ø	ery	61.1	52.0	37.2	34.5	21.1	14.0	7.8	7.7	7.1	7.1	7.0	7.0	6.9	6.9	6.9	9.8	6.8	6.8	6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9
	Score	818	969	498.5	462.5	283	188	105	103			93.5		92	92	92	91.5	91	90.5	90	90	89.5		68	68		88.5			88
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hypothetical prote probable splicing	probable RNA helic	FUSION, methionine	reticulocyte-bindi	aldehyde dehydroge	hypothetical prote	probable membrane	clathrin heavy cha	conserved hypothet	homoserine dehydro	phosphoprotein pho	hypothetical prote	lipoprotein [impor	inter-alpha-inhibi	hypothetical prote
T33065 SE0096	\$63453	E96935	A42771	A83758	T17243	S64384	A36349	D86715	AC1393	T45058	A82488	H90514	S54354	S45872
~ -	4 72	N	~	~	N	7	N	(7)	N	-	N	N	N	7
495	737	596	2829	452	701	936	1653	265	428	526	638	843	946	918
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9.4		9	9	G	Ψ	Ψ	_	•	·	w	w	w	_	
9.9	88		87.5 6							96			86	85.5

## ALIGNMENTS

RESULT 2 838958 chorismate mutase (EC 5.4.99.5) precursor - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 07-Mar-2003

N

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6

Indels

84; DB 2;

Length 256;

77 68 189

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A,Pathway: aromatic amino acid biosynthesis
C,Superfamily: chorismate mutase of the AroQ class, eukaryotic type
C,Keywords: aromatic amino acid biosynthesis; intramolecular transferase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELLPL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKY--AQIQGFCGSLVEFVVKNTE
                                                                                                                                                                                                                                                                                                                                         9 VINLQNIRDELVRMEDSIIFKFIERSHFATCPSVYEANHDGLEIPNFKGSFLDWALSNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LA-TSGDD-GNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYBPLIRAKDKEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLTFTSVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLYKNWVIPLTK
                                                                                                                                                 37.2%; Score 498.5; DB 40.5%; Pred. No. 6e-33; tive 57; Mismatches
                                                                                                                                                     Query Match
Best Local Similarity 40.5%
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 EVEVEYLLRRLE 255
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Best Local Similarity
Matches 98; Conserv
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NAAlternate names: protein YP9499.15c; protein YPR060c
C; Species: Saccharomyces cerevisiae
C; Daces Saccharomyces cerevisiae
C; Daces Saccharomyces cerevisiae
C; Daces Saccharomyces cerevisiae
C; Daces Saccharomyces cerevisiae
C; Daces Saccharomyces cerevisiae
C; Daces Saccharomyces cerevisiae
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                                   Eberhard, J.; Raesecke, H.R.; Schmid, J.; Amrhein, N.
BBS Lett. 334, 238-236, 1993
Fitle: Cloning and expression in yeast of a higher plant chorismate mutase. Molecular
Reference number: S38958; MUID:940,3841; PMID:8224252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathway: aromatic amino acid biosynthesis
Superfamily: chorismate mutase of the ArcQ class, eukaryotic type
Keywords: aromatic amino acid biosynthesis; chloroplast; intramolecular transferase;
11-60/Pomain: transit peptide (chloroplast) #status predicted <TNP>
61-334/Product: chorismate mutase #status predicted <MAT>
                                                                                                      A,Title: Cloning and expression in yeast of a higher plant chorismate mutase..MA, Title: Cloning and expression in yeast of a higher plant chorismate mutase..MA, Reference number: S38958; MUID:94039841; PMID:8224252
A,Accession: S38958
A,Molecule type: mRNA
A,Residues: 1-334 <EBE>
A,Cross-references: EMBL:226519; NID:9429152; PIDN:CAA81286.1; PID:9429153
C,Genetics:
C,Genetics: A,Genome: nuclear
C,Function:
A,Description: intramolecular transferase; isomerase
A,Bethway: arcmatic amino acid biosynthesis
C,Superfamily: chorismate mutase of the AroQ class, eukaryotic type
C,Keywords: aromatic amino acid biosynthesis; chloroplast; intramolecular trans
F;1-60/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;61-334/Product: chorismate mutase #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLTFTSVEBTVRKRVEKKAVVFGQEVNLNSDDNDNENR-----KFDPSVASSLYK 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%; Score 696; DB 2; Length 334; larity 50.4%; Pred. No. 9.1e-49; Conservative 46; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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A,Residues: 1-251 <OLI>
A,Cross-references: EMBL:298529; PIDN:CAB11033.1; GSPDB:GN00066; SPDB:SPAC16E8.04c
A,Experimental source: strain 972h-; cosmid c16E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 TSGDD-GNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                    C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAKAGRYKNPEENAFFPENLPPSIVPSYSFKOFLHPGAASININKSIWKMYFKELLPLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 LIFISVEETVRKRVEKKAVVFGQEVNLNSDDNDNENRKFDPSVASSLYKNWVIPLIKEVQ
probable chorismate mutase - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                              A;Introns: 231/3
C;Superfamily: chorismate mutase of the AroQ class, eukaryotic type
                                                                                                                                                                                                                                                                                                                                                                                                            Length 251;
                                                         C,Accession: T37784
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, submitted to the EMBL Data Library, September 1995
A;Reference number: 221746
A;Accession: T37784
A;Staus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-251 < OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                        34.5%; Score 462.5; DB 2;
ilarity 39.5%; Pred. No. 4.8e-30;
Conservative 54; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 VDYLLARL 250
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A;Cross-references: SGD:S0006264; MIPS:YPR060c A;Map position: 16R C:Punction: intramolecular transferase; isomerase A;Description: intramolecular transferase; isomerase

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Desired the morphilus influenzae (EC 1.17.4.1) alpha chain - Haemophilus influenzae (Species: Haemophilus influenzae (Species: Haemophilus influenzae (Species: Haemophilus influenzae (Species: Haemophilus influenzae (Species: Haemophilus influenzae (Species: Haemophilus influenzae (Species: Haug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999 (Species: Baya-1995 #sequence_revision: B64135 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Scott, J.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995 A.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. A.; Reference number: A64000; MUID:95350630; PMID:7542800 A.; Molecule whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A.; A.; Atatus: nucleic acid sequence not shown; translation not shown A.; Molecule type: DNA A; Residues: 1-781 crIGR>
A; Molecule type: DNA A; Residues: 1-781 crIGR>
C; Genetics: GB:U32839; GB:L42023; NID:g1574508; PIDN:AAC23305.1; PID:g1574509; T)
                                     "Mypothetical protein SP0355 [imported] - Streptococcus pneumoniae (strain TIGR4)
C'Species: Streptococcus pneumoniae
C'Species: Streptococcus pneumoniae
C'Species: Streptococcus pneumoniae
C'Spaces Sion: G95041
B'Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I nson, T.; Hickey, E.K.; Holt, I.E.
A'Authors: Loftus, B.J.; Mang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: Asequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; WUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:AAK74528.1; PID:g14971828; GSPDB:GN00164; TIGR:SP48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : : : | | : : : | : | | : : | : | | | : : : : | | | : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 TAANDLSLLQSISRRIHYGKFVAEVKFRD------AP--QDYEPLIRAKDKEGLM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: herpesvirus ribonucleoside-diphosphate reductase large chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 EENAFFPENLPPSIVPSYSFKOFLHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 IVYDLLESKGYEVSFYNPSDFFQMYLKEYRQKQ-----SFTKKQADALLYIPGGYFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GHNARFRDNL-----IQFKRFLPLG------IWASYFKKPIGVLGIGAGPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 IIYGLIERAKF-----PSN-SHTYDEKYAQIQGFCGSLVEFVVKNTEAIQAKAGRYKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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C,Superfamily: herpesvirus ribonucleoside-diphosphate reductase
C,Keywords: DNA replication; iron-sulfur protein; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
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22.9%; Pred. No. 2.7;
tive 36; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.8%; Score 105; DB 2; Length 360 Best Local Similarity 24.7%; Pred. No. 0.64; Matches 55; Conservative 34; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 KLLTFTSVEETVRKRV-----EKKAV-VFGQEVNLNSDDNDN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
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A, Experimental source: strain TIGR4
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A,Molecule type: DNA
A,Residues: 1-360 <KUR>
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Best Local 8
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C.Species: Petroselinum crispum (parsley)
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 07-Mar-2003
C.Accession: T14901
R.Bat. Logemann, E.; Reinold, S.; Hahlbrock, K.
Submitted to the EMBL Data Library, July 1997
A.Description: Extensive reprogramming of cellular metabolism by fungal elicitor or infe A.Accession: T14901
A.Accession: T14901
A.Molecula type: mRNA
A.Mosiques: 1-70 cBAT>
A.Molecule type: mRNA
A.Resiques: 1-70 cBAT>
A.Ross-references: EMBL:AF012866; NID:g2352928; PID:g2352929
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chorismate mutase (EC 5.4.99.5) 2, cytosolic - parsley (fragment)
C;Species: Petroselium crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 07-Mar-2003
C;Accession: T14902
R;Batz, 0.; Logemann, E.; Reinold, S.; Hahlbrock, K.
submitted to the EMBL Data Library, July 1997
A;Description: Extensive reprogramming of cellular metabolism by fungal elicitor or: A;Reference number: 218251
A;Accession: T14902
A;Accession: T14902
A;Gestion: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:AF012867; NID:g2352930; PID:g2352931
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C;Function:
A;Description: intramolecular transferase; isomerase
A;Description: aromatic amino acid biosynthesis
C;Superfamily: chorismate mutase of the AroQ class, eukaryotic type
C;Keywords: aromatic amino acid biosynthesis; intramolecular transferase;
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21.1%; Score 283; DB 2; Length 82;
Best Local Similarity 63.4%; Pred. No. 3.4e-16;
Matches 52; Conservative 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th 14.0%; Score 188; DB 2; Length 70; Similarity 51.4%; Pred. No. 1.3e-08; 36; Conservative 8; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 DLSLLQSISRRIHYGKFVAEVK 169
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A;Genome: nuclear
C;Function:
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probable membrane protein YFR041c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein F018
N;Alternate names: hypothetical protein F018
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence revision 19-Oct-1995 #text_change 23-Sep-2002
C;Accession: 856296; 862252; 863788
R;Murakami, Y; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanum A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces cen A;Reference number: 856186
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A; Residues: 1-295 cMUM-
A; Residues: 1-295 cMUM-
A; Crestances: 1-295 cMUM-
A; Crestances: EmBi.D44597; NID: 9871938; PID: d1008597; PID: 9871940
R; Ext. T.; Natrou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, N
Yeast 12, 149-167, 1996
A; Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome V3
A; Reference number: S63787; MUID: 96287652; PMID: 8686379
          A;Accession: S59393
A;Molecule type: DNA
A;Rosidues: 1-1556 <JOH>
A;Rosidues: 1-1556 <JOH>
A;Cross-references: EMBL:U20865; NID:g662330; PID:g662344; GSPDB:GN00012; MIPS:YLR247c
A;Experimental source: strain S288C (AB372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Wolecule type: DNA
;Residues: 1-295 <MUR>
;Cross-references: EMBL:D50617; NID:g836685; PID:d1009921; PID:g836796; MIPS:YFR041c
                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLIDPILANSDELQAMGRNNRIG------QDEETFVWNFMIRNTVEENILRYKC 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 -- QGPCGSLVEFVVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAAS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEP----LIRAKDKEGLMKLLT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 FISVEETVRKRVEKKAVVFGQBVNLNSDDNDNE---NRKFDPSVASSLYKNWVIPLIKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KAAEQSPDSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQI
                                                                                                                                                                                                                                                                                                                                                                                       Length 1556;
                                                                                                                                                                                                                                                      C;Superfamily: RING finger homology
C;Reywords: transmembrane protein
F;1235-1282,Domain: RING finger homology «RRN»
F;1236-1252/Domain: transmembrane #status predicted <TVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NYAQTAA---
                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murakami, Y.

ubmitted to the BMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Score 95.5;
Pred. No. 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ININKSIWKMYFKELLPLLATSGDDG-
                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 21.3%;
Matches 65; Conservative 4
                                                                                                                                                                         A,Gene: MIPS:YLR247c
A,Cross-references: SGD:S0004237
A,Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: S62230; Accession: S62252
  A;Reference number: S59386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1543 SNEHL 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 QVEYL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S56296
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K.;
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ano, T.; Inoue, R.; Kaito, C.; Sekimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule Type: DNA

A; Mesiduces: 1-597 - KMDs.

A; Mesiduces: 1-597 - KMDs.

A; A; Cross-references: GB: BA000018; PID: g13702378; PIDN: BAB43519.1; GSPDB: GN00149

A; Experimental source: strain N315

C; Genteics: A; Gente: SA2217

C; Superfamily: beta-1, 2-glucan export protein chvA; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 YPQTAVKSCSQGGVRGGAATLYY--PIWHLEAENLLVLKNNRGVEDNRVRHMDYGVQLNK 366
                                                                                                                                                                                                                                424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 GYMNLGASVLPS-TFLGILPVGMYLISINQLNYABFFLCIVLSLGVVAPIKNFTNYVNHL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
                                                                            FKQF-----LHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIR-----AKDKEGLM-KLLTFT-- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SVEETVRKRVEKKAVVFGQEVNLNS-DDNDNENRKFDPSVASSLYKNW 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423
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859393
Probable membrane protein YLR247c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein L9672.14
C;Species: Saccharomyces cerevisiae
C;Species: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 KSIQYALTEVNQILSLEBLVLSTKFK-KPQHYEIAFNNVGFSYNKDKDDLVFKHLSFTVP
                                                                                                                                                                                                                   : | : | : | : | : | : | 367 LMYQRLIKGSEITLFSPSDVPGLYEAFFADQDK--FEELYVKYEQDPTIRKRTVKAVEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 ENNFTAIVGASGSGKSTIAKLISRYWDVTSGEITIGGINIKDIESKQLNDLVGFVGQDNF
                                                                                                                                                                                  154 SISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKLLTFTSVEETVRKRVEKKAVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHIYDEKYAQIQGFCGSLVEF----VVKNTEAIQAKAGRYKNPEEN-----AFFPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NLPPSIVPSYSPKOFLHPGAASININKSIWKMYFKEL---LPLLATSGDDGNYAQTA
                                                                                                                                                                                                                                                                                    214 G---QE-----TKEVQ 252
                                                                                                                                                                                                                                                                                                                7.1%; Score 95.5; DB 2; Length 587; 22.9%; Pred. No. 7.4; tive 45; Mismatches 101; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S59393
R;Johnson, D.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of S. cerevisiae cosmid 9672.
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Conservative

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Similarity

Local Best Loc Matches

Query Match

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Cispecies: Rickettsia prowazekii
Cispecies: Rickettsia prowazekii
Cispecies: Rickettsia prowazekii
Cispecies: Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
Circession: A71683
Richadersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A; Thile: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A; Reference number: A71630; MUD:99039499; PMID:9823893
A; Reference number: A71630; MUD:99039499; PMID:9823893
A; Reference number: A71630; Mulo:eic acid sequence not shown; translation not shown
A; Residues: 1-371 cAND>
A; Residues: 1-371 cAND>
A; Residues: 1-371 cAND>
A; Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14739.1; PID:g386083: A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 PSYSFKQF------LHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQTAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 NDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKLLTFTSVEETVRKRV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 KELEKLQEIVSKIEYSK---KSKTND-----IIINNPNSTVVKNLLKEKIDEKISSKE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 -PSNSHTYDEKYAQIQGFCGSLV--EFVVRNTEAIQAKAGRYKNPEENAFFPENLPPSIV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane protein YGR103w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G5933
C;Species: Saccharomyces cerevisiae
C;Species: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 PIY--KQMDEEREELFKLAEILPQYAQANIDKHA-KLYAKQYQTKIE---NDPNY----
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R;Hernandez, K.; Weber, N.; Wipfli, P.; Schmidheini, T.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64392
A;Accession: S64408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
6.9%; Score 92; DB 2; Length 371;
Best Local Similarity 22.6%; Pred. No. 7.5;
Matches 64; Conservative 34; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 EKKAV-VFGQEVNLNSDDNDNENRKFDPSVASSLYKNWVIPLT 248
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1996
                                                                                                                                                                                                       hypothetical protein RP278 - Rickettsia prowazekii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C)Accession: S64410, S64408
C)Accession: S64410, S64408
E) Wedler, H.; Scharfe, M.; Wedler, E.; Wambutt, submittor the Protein Sequence Database, May A; Reference number: S64356
A; Accession: S64410
A; Modecule type: DNA
A; Residues: 1-605 <WED>
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A;Residues: 1-18 <HER>
A;Cross-references: EMBL:Z72888; MIPS:YGR103w
A;Experimental source: strain S288C
C;Genetics: A;Genetics:
             | :|| : : | : | : | 199 LRELLAYKGISTREHELKSEIDKLSV 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VYTLASVREDLVRQEDTIIYGLI--
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C,Species: Pyrococcus abyssi

C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C,Accession: D75014

R,anonymous, Genoscope

Submitted to the EMBL Data Library, July 1999

A,Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A,Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: preliminary
A Molecule type: DNA
A Molecule: 1-1134 «KM»
A Cross-references: GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB50554.1; PID:e151645
A Experimental source: strain Orsay
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 AKAGRYKNPEENAFFPE-NLPPSIVPSYS----FKOFLHPGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 KKYHPDKAPKYRKIYERLATQILSNSSNRKIYDYYLQNGFPNYDFHKG--GFYFSRMK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P----LLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 KEGL-MKLLTFISVEETVRKRVEKKAVVF------GQEVNLNSDDNDNENRKFDP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 GRYKNPEENAFFPENLPPSIVPSYSFKOF--LH-----PGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 PLLATSGDDGNYAQTAANDLSL-LQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 YAFTIETEIFQLQNEI-----STKYGPDMNFY--KFLKLPKLQNSSTKEITKNIRKLS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 YTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKNTEAIQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
18 ASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKNTEAIQAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
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                                                                                                                                                                                                                                                                                                                                                                                              7.0%; Score 93.5; DB 2; Length 295; 22.1%; Pred. No. 4.2; tive 42; Mismatches 96; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754 SRIGİNIEVKTLDNIRLGDLDISLEDIAKK---
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Matches 56, Conservative
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Best Local Similarity 22.8
Matches 47; Conservative
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202 KQEMLSVLSVRERLEKALSFWEAEISVLQVEKRIRSRVKRQMEKTQREYYLNEQMKAIQK 261
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                                                                                                                                                                                                              ----SDDNDNENRKFDPSVASSLYKNWVIPLTKEVQVEYL--LRRL
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     176 DYEPLIRAKDKEGLMKLLTF---
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 02-Jun-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AAEQSPDSGNVY---TLASVREDLVRQEDTIIYGLIE---RAKFP--SNSHTYDEKYAQI
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                                                                                                                                                                                                                                                                                                                                                                                                           74; Gaps
                                                                                                                                                                                                                                                                               6.9%; Score 92; DB 2; Length 605; llarity 20.5%; Pred. No. 15; Conservative 50; Mismatches 116; Indels
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A,Cross-references: SGD:S0003335
A,Map position: 7R
C;Keywords: transmembrane protein
F;217-233/Domain: transmembrane #status predicted <TMM>
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6.9%; Score 92; DB 2
Best Local Similarity 22.0%; Pred. No. 22;
Matches 63; Conservative 44; Mismatches
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C,Superfamily: ATP-dependent Lon protease
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Best Local Similarity
Matches 62; Conserv
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C;Accession: AF3361
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OM protein - protein search, using sw model

September 25, 2004, 01:26:35; Search time 18 Seconds (without alignments) 755.017 Million cell updates/sec Run on:

US-10-624-061-16 1339 1 MAKAAEQSPDSGNVYTLASV......NWVIPLTKEVQVEYLLRRLD 261

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		~	_	P43754 haemophilus			saccharom		P53261 saccharomyc	Q8yhc6 brucella me	Q8g0i7 brucella su				Q9phl0 campylobact						Q919i7 salmonella					P22137 saccharomyc	_		_	ther	rana ric	O71024 african hor	P40556 saccharomyc
SUMMARIES		DI				RIR1 HAEIN	SUV3_SACDO		YFL1 YEAST	LON BRUAB	PESC_YEAST	LON BRUME	LON BRUSU	ATPA BUCAP	THIC_SALTI	ALP6 SCHPO	HSLU_CAMJE	HAP4_YEAST	BFG_STRMU	ITHZ MESAU	RPOB_AQUAE	SUV3 YEAST	THIC_SALTY	CAD9 HUMAN	RBP1_PLAVB	CDB5_HUMAN	YG2K YEAST	CLH YEAST	ITHZ_MOUSE	IMB2_YEAST	COMO_BACSU	ARGJ THETH		VP2 AHSV6	YIA6_YEAST
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 TEKLHAKVGREKSPDEHPFFPDDLPEPMLPPLQYPKVLHFAADSININKKIWMYFRDLV 194
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MEDLINE=9731321; PubMed=9169875;
MEDLINE=9731321; PubMed=9169875;
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
Chung B., Churcher C.M., Coster F., Davis K., Davis R.W.,
Dietrich F.S., Delius H., Dispaolo T., Dubois E., Duesterhoeft A.,
Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.1%; Score 698; DB 1; Length 334; Best Local Similarity 50.4%; Pred. No. 2.8e-47; Matches 131; Conservative 46; Mismatches 75; Indels
                                                                                                                    InterPro; IPR008238; Chor mut AroQ eu.
InterPro; IPR008951; Chorismat mut II.
InterPro; IPR007701; Chorismate mut.
Pfam; PF01817; Chorismate mut.
PIRSF; PIRSF017318; Chor mut AroQ eu; 1.
Aromatic amino acid biosynthesis; Isomerase; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                  CHORISMATE MUTASE.
A -> R (IN REF. 1).
4D477B08E349B08C CRC64;
                                                                                                                                                                                                                                                                                                                                                       CHLOROPLAST (POTENTIAL).
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01-OCT-1993 (Rel. 27, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-3003 (Rel. 42, Sequence update)
ARO7 OR OSM2 OR YPROGOC OR YP9499.15C.
                                                                                                                                                                                                                                                                                                                        Transit peptide, Allosteric enzyme.
TRANSIT 1 60 CHLOROE
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MEDLINE=89155418; PubMed=2646272;
EMBL; AJ242647; CAB54518.1; -. EMBL; AB026657; BAB01816.1; -. PIR; S38958; S38958.
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334 AA; 37594 MW;
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                                                                                                HSSP; P32178; 5CSM
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Romp C., Kutti O., Lambhari D., Law H., Lin A., Lin D., Louis E. J., Marathe R., Wesserguy P., A., Mittipaci S., Woesto D., A., Marathe R., Wesserguy P., Wewes H.-W., Mittipaci S., Woesto D., Mallet-Ates S., Mealer D., Law H., Lin A., Lin D., Louis E. J., Mallet B., Moster B., Mallet B., Moster B., Mallet B., Moster B., Mallet B., Moster B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Will Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mallet B., Mal
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ROD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bagouros U., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bagouros U., Barown S., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., Callins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gallies M., Connor R., Chones P., Hadlgo J., Hodgson G., Anderse S., Goble B., Mundler S., McDean J., Rames K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Noule S., Mundler S., McDean J., Rames K., Jones L., Jones M., Leather S., McDonald S., McLean J., Rabelton U., Simmonds M., Squares R., Squares R., Squares R., Staren T., Whitehead S., Rucherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller H., Reinhardt R., Pohl T.M., B. Borzym K., Langer I., Beck A., Iehrach H., Reinhardt R., Pohl T.M., A. Gaffeau A., Cadieu E., Dreano S., Gloux S., Lenner V., Mottier S., Albert E., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Cruzado L., Jümene S., Gloux S., Lenner M., Gallardin J., Sanchez M., Galzon A., Garzon A., Bonito J., Morone Sequence of Schizosaccharomyces pombe.";

RA Daga R.R., Cruzado L., Jümene J., Sanchez M., Galzon J., Potashkin J., R. Shpakovski G.Y., Usery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

RA Gribert F. PAWER B. Schwett P., Brenklin W. R., Pelhenate C. C., PARLYTIC ACTIVITY: Chorismate = prephenate

C. -- RARLYTIC ACTIVITY: Chorismate = prephenate

C. -- Subnit B. Boodwart C. Alleria Blosymtherity Proportion C. -- Subnit B. C., Nurse B. C. Schizosaccharomyces domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 QAKAGRYKUPEENAFFPENLPPSIVPSYSFKQFLHPGAASININKSIWKMYFKELLPLLA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPGDDFDNYGSTVVCDIRCLQSLSRRIHYGKFVAEAKYLANPSKYKKLILARDIKGIENE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 LASVREDLVRQEDTIIYGLIERAKFPSNSHTY---DEKYAQIQGFCGSLVEFVVKNTEAI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 TSGDD-GNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LENIRSALIRQEDTIIFNFLERAQFPRNEKVYKSGKGCLNLENYDGSFLNYLLHEEEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01817; Chorismate_mut; I.
PIRSF; PIRSF017318; Chor_mut, AroQ eu; 1.
Aromatic amino acid biosynthesis; Isomerase.
SEQUENCE 251 AA; 29050 MW; 1AC18AE4C1E6C4B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%; Score 462.5; DB 1
Local Similarity 39.5%; Pred. No. 4.5e-29;
les 98; Conservative 54; Mismarch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P32178; ECSM.
GeneDB SPombe; SPACIERS.04c; -.
InterPro; IPR008238; Chor mut AroQ eu.
InterPro; IPR008951; Chorismat mut II.
InterPro; IPR008951; Chorismate mut II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z98529; CAB11033.1; -. PIR; T37784; T37784.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VINLONIRDELVRMEDSIIFKFIERSHFATCPSVYEANHPGLEIPNFKGSFLDWALSNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 VYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKY--AQIQGFCGSLVEFVVKNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 AIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKOFLHPGAASININKSIWKMYFKELLPL
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 498.5; DB 1
Pred. No. 7.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHMU_SCHPO STANDARD; PRT; 251 AA. 013739; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-2003 (Rel. 42, Last annotation update) Probable chorismate mutase (EC 5.4.99.5) (CM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.2%; Scc. No. /...
40.5%; Pred. No. /...
.... 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.5
Matches 102; Conservative
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SEQUENCE FROM N.A.
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셤 ò INTERACTS WITH THIOREDOXIN/GLUTAREDOXIN

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11]

SEQUENCE FROM N.A.

STRAINER OF WELL STATES 1907;

WEDLINE=95350630; PubMed=7542800;

REDLINE=95350630; PubMed=7542800;

REDLINE=95350630; PubMed=7542800;

RELINE=95350630; PubMed=7542800;

RELINE=95350630; PubMed=7542800;

Reline N.D., Reline N.D., Ritzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Luu L.-I., Glodek A., Kelley J.W.,

Reidman J.F., Phillips C.A., Ngyraps T., Hedblom E., Cotton M.D.,

Reidman J.F., Phillips C.A., Ngyraps T., Hedblom E., Cotton M.D.,

Reidman J.F., Phillips C.A., Suprings T., Hedblom E., Cotton M.D.,

Reidman J.F., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Reidman J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Nonter J.C.;

Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides, precursors that are necessary for DNA synthesis (By similarity).

CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized thioredoxin + H(2)O = ribonucleoside diphosphate + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
SIMILARITY: Belongs to the ribonucleoside diphosphate reductase
large chain family.
                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)
                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: DNA replication pathway; first step. SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                            756 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32839; AAC23305.1; ALT INIT.
HSSP; P00452; SRIR.
                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                     (Ribonucleotide reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995)
                                                                                                           STANDARD;
                                                                                                                                                                                                                                 Haemophilus influenzae
VEYLLRRL 260
                   |:||| ||
243 VDYLLARL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thioredoxin.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                                  NRDA OR HI1659
                                                                                                                                     01-NOV-1995 (
01-NOV-1995 (
28-FEB-2003 (
                                                                                                           HAEIN
253
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                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                231 DDSLDSINATASAIVKYVSQRAGIGINAGAIRALGSEIRGGE--ÀFH-----TGCIPFYK 283
                                                                                                                                                                                                                                                                                                                                                        103 FKQF------LHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQ 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 LMYQRLIKGSEITLFSPSDVPGLYBAFFADQDK--FEELYVKYEQDPTIRKRTVKAVEIF 399
                                                                                                                                                                                                                                       49 DEKYAQIQGPCGSLVEFVVK-----NTEAIQAKAGRYKNPEENAFFPENLPPSIVPSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 SISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKLLTFTSVEETVRKRVEKKAVVF
                                                                                                                                                                                                                                                                                                                                                                                                             284 YFOTAVKSCSOGGVRGGAATLYY--PIWHLEAENLLVLKNNRGVEDNRVRHMDYGVOLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 G---OB----TKEVD DNDNENRKFDPSVASSLYKNWVIPL---TKEVQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 SLLMQERASTGRIYIQNVDHCNTHSPFDPQVAPVRQSNLCLEIALPTKPLQ 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRION (POTENTIAL), ATP-DEPENDENT RNA HELICASE SUV3.
                                                                                                                   Length 756;
                                                                                                                   Score 103; DB 1; Length 75
Pred. No. 1.9;
5; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-0CT-2003 (Rel. 42, Last Sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
ATP-dependent RNA helicase SUV3, mitochondrial precursor.
                                                        839D02FA61E185D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P (POTENTIAL).
E24DD4C2097CA961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     737 AA
                               SIMILARITY
                                                                                       7.7%; Suc. 22.9%; Pred
                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces douglasii (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AJ011586; CAA09716.1; -.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
                                                        85695 MW;
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                                                           756 AA;
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                                                                                                                                                Similarity
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NP BIND
SEQUENCE
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                                                                                                                   Query Match
                                                                                                                                                Best Local
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SUV3_SACDO
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DB 1; Length 737;

7.5%; Score 101;

Query Match

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InterPro, IPR008926; Ribonucleo_red_N.
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SEQUENCE
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                                                                                                                                                                                                                                 SEQUENCE
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P43613;
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                         18;
                                                                                                                                                                                                                    225
                                                                                                                                                                                                                                                                       226 BARKIRRHIIMHIGP-----TNSGKTYRALQKLKSVDRGYYAGPLRLLA-REVYDRPQ 277
                                                                                                                                                                                                                                                                                                                                               278 SEKVRCNILTGEEVIRDLDDKGNPAGLTSGTVEMVPINOKFDVVLDEIQMMSDADRGWA 337
                                                                                                                                        K-----RYFKELLPLLATSGD-DGNYAQTAAND---LS 150
                                                                                                                                                                                                                                                    151 LLQSISRRI--HYGKFVAEVKFRDAPQDYEPLIRAKDKE-----GLMKLLTFTSVEETVR 203
                                                                                                                                                                                                                                                                                                                  204 KRVEKKAVVFGQEVNLNSDDNDNE------NRKFDPSVASSLY-----KNW- 243
                                                                                EALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKOFLHPGAAS-----ININK---SIW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=2246501; PubMed=1252265;
MEDLINE=2246501; PubMed=1252265;
MEDLINE=2246501; PubMed=12522265;
MEDLINE=2246501; PubMed=1252265;
MEDLINE=2246501; C. H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
Trangencive genome evolution in Buchnera aphidicola.";
Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
-: FUNCTION: Catalyzes the biosynthesis of deoxyribonucleotides from
the corresponding ribonucleotides, precursors that are necessary
for DNA synthesis (By similarity).
-: GATALYTIC ACTIVITY: 2' deoxyribonucleoside diphosphate + oxidized
thioredoxin + H(2)O = ribonucleoside diphosphate + reduced
                                                                                                                                                                                                        SGNYYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVRNT
                         93; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the ribonucleoside diphosphate reductase large chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thioredoxin.
PATHWAY: DNA replication pathway; first step.
SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761 AA
           Pred. No. 2.7;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     ----VIPLTKEV 251
                                                                                                                                                                                                                                                                                                                                                                                                                  338 WINALLGVVSKEVHLVGEKSVLPLVKSI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR005144; ATP.
Interpro; IPR000788; Ribonucleo_red.
20.1%; Fi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Ribonucleotide reductase).
NRDA OR BBP168.
                              66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
           Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=135842;
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089AS4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 RRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKLLIFTSVEETVRKRVEKKAVVFG-- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|: |: :| |: :| | | |: :| 345 QRLILGEHITLFSPSDVPNLYDSFFNNQEK--FBRLYIKYENDKTIRKKKVKASYLFSLM 402
                                                                                                                                                                                                                                                                                                                                                                         49 DEKYAQIQGFCGSLVEFVVKNTEAIQAKAGRYK---NPEENAFFPENLPPSIVPSYSFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                 231 BDNLNSINATTSALVKYVSQRA-GIGINAGRIRALGSPIRNG---DTLHTGCIPFYKHFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 SAVKSCSQGGVRGGAATIFY--PIWHFEIESLLVLKNNRGIEENRVRHMDYSVQLNKLMY
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                           INTERACTS WITH THIOREDOXIN/GLUTAREDOXIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y., Analaysis of a 56.2 kb DNA sequence including the right telomere chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Ssaanuma S.-I., Saanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-PED-2003 (Rel. 41, Last amnotation update)
Hypothetical 34.2 kDa protein in SAPI55-YMR31 intergenic region
                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                 DB 1; Length 761;
                                                                                                                                                                                                                                                                                                                    20.8%; Pred. No. 9;
Live 42; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 MQERTSTGRIYIQNVDHCNSHSAFNPKIAPIRQSNLCLEIT 443
                                                                                                                                                                                                                                                         7FB14E136283BDCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 -QE-----VNLNSDDNDNENRKFDPSVASSLYKNWVIPLT
Pfam; PF03477; ATP-cone; 1.
Pfam; PF003177; ATP-cone; 1.
Pfam; PF00317; ribonuc_red_lg; 1.
PR01183; RIBORDTASEM1.
PROSTTE; PS00089; RIBORED_LARGE; 1.
PROSTTE; PS00089; RIBORED_LARGE; 1.
ACT_SITE 225 225 BY SIMILARITY.
ACT_SITE 439 439 BY SIMILARITY.
ACT_SITE 462 BY SIMILARITY.
ACT_SITE 754 754 INTERACTS WITH T
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                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                 Score 94.5;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 J domain.
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STRAIN=S288c / AB972;
MEDLINE=96287652; PubMed=8686379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-5288C / AB972;
MEDLINE-95400292; PubMed=7670463;
                                                                                                                                                                                                                                                             87124 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995)
                                                                                                                                                                                                                                                                                                     7.18;
                                                                                                                                                                                                                                                                                                                      Local Similarity 20.8
les 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                       759
                                                                                                                                                                                                                                                               761 AA;
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EMBL; AF042348; AAB97420.1; -. MEROPS; S16.001; -.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to peptidase family S16.

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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 AKAGRYKNPEENAFFPE-NLPPSIVPSYS----FKQFLHPGAASININKSIWKMYFKELL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 YTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKNTEAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 KKYHPDKNPKYRKLYERLNLATQILSNSSNRKIYDYYLQNGFPNYDFHKG--GFYFSRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P----LLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEGL-MKLLTFTSVEETVRKRVEKKAVVF------GQEVNLNSDDNDNENRKFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
HYPOTHETICAL PROTEIN YFR041C.
J-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 93.5; DB 1; Length 2
; Pred. No. 3.3;
42; Mismatches 96; Indels
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                                                                                                                                                                                                                                                          EMBL, D50617, BAA09280.1; -.
PIR. S56296, S56296.
Germonline; 140195; -.
SGD; S0001937; YER041C.
InterPro; IPR001623; DnaJ N.
InterPro; IPR00305; Hsp_DnaJ.
PEM, PF00226; DnaJ. I.
PRINTS; PR00625; DNAJPROTEIN.
SWART; SW00271; DnaJ: 1.
PROSITE; PS00636; DNAJ-1; 1.
PROSITE; PS00636; DNAJ-2; 1.
Hypothetical protein; Ghaperone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 AA; 34191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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InterPro; 1PR00359; AAA ATPase.
InterPro; 1PR00359; AAA ATPase.
InterPro; 1PR00359; AAA ATPase centr.
InterPro; 1PR00320; Pept side cip.
InterPro; 1PR004815; Pept Side C.
InterPro; 1PR004815; Pept Side C.
InterPro; 1PR004815; Pept Side AS.
InterPro; 1PR009269; Peptid Side AS.
InterPro; 1PR009269; Peptid Side AS.
InterPro; 1PR001964; Peptid Side AS.
InterPro; 1PR001964; Peptid Side AS.
InterPro; 1PR001964; Peptid Side AS.
InterPro; 1PR001969; Deptid Side AS.
InterPro; 1PR001969; LON; 1.
Pfam; PF00380; LON C.; 1.
PRNAT; SN00382; AAA; 1.
SWART; SN00464; LON; 1.
PR081RE; PR00166; LON; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.
PR081RE; PS001046; LON SER; 1.

367 374 ATP (POTENTIAL). 689 689 BY SIMILARITY. 812 AA: 89859 MW, B9D07E9F0D7EPBB CRC64;

ACT SITE SEQUENCE

NP BIND ACT

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56 QGFCGSLVEFVVKNTEAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASIN 115
                                                                                                                                                                                                                               116 INKSIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQ 175
                                                                                                                                                                                                                                                                                                                                              191 KQEMLSVLSVRERLEKALSFMEAEISVLQVEKRIRSPVKRQMEKTQREYYLNEQMKAIQK 250
                                                                                                                                                                                 4 AAEQSPDSGNVY---TLASVREDLVRQEDTIIYGLIE---RAKFP--SNSHTYDEKYAQI
                                                                                                                                                                                                                                                                                                        176 DYEPLIRAKDKEGLMKLLTF-----TSVEETVRKRVEKKAVVFGQEVNLN------
                                                                                                                AADDDPAPDAIYEIGTIANVLQ-LLKLPDGTVKVLVEGTARAKISKFTDREDYHEAYA--
                                          94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pescadillo homolog.

NOP7 OR RRP13 OR YPH1 OR YGR103W.
Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                   155 LNKKI----SPEVVGAASQIDDYSKLADTVASHLAI----SPEVVGAASQIDDYSKLADTVASHLAI----
                                                                                                                                                                                                                                                                                                                                                                                  ----SDDNDNENRKFDPSVASSLYKNWVIPLTKEVQVEYL--LRRL 260
                                                                                                                                                                                                                                                                                                                                                                                                          |:| :| : | ::| 251 ELGDSEDGRDEVAEIEERITKT-----KLSKEAREKALAELKKL 289
      DB 1;
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
  6.9%; Score 93; DB 1
22.0%; Pred. No. 13;
ative 44; Mismatches
                                      63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
Query Match
Best Local Similarity
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P53261;
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Robertson G.T., Kovach M.E., Allen C., Ficht T.A., Roop R.M. II;
Submitted (JAN-1998) to the EMBL/Genbank/DDBJ databases.
-!-FUNCTION: Degrades short-lived regulatory and abnormal proteins in
presence of ATP. Hydrolyzes two ATPs for each peptide bond cleaved
in the protein substrate (By similarity).
-!-CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin,
casein and denaturated serum albumin, in presence of ATP.
-!-SUBUNIT: Homotetramer (By similarity).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.

Brucella abortus.

SEQUENCE FROM N.A.

WCBI\_TaxID=235;

LON BRUMB

10 LON BRUMB

10 LON BOT 15-DB DT 15-

15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP-dependent protease La (EC 3.4.21.53).

STANDARD;

LON BRUAB 052605;

375 IL 376

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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

RA SEQUENCE FROM TACC 23456 / Biotype 1;

RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

RA DelVecchio V.G., Kapatral V., Redkar R.J., Lykidis A., Reznik G.,

RA Jablonski L., Laren N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Jablonski L., Larens N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Jaselkorn R., Kyrpides N., Overbeek R.;

RA Haselkorn R., Kyrpides N., Overbeek R.;

RT Fre genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

RT Brucella melitensis.";

RT Brucella melitensis.";

C. -: FUNCTION: Degrades short-lived regulacory and abnormal proteins in

CC -: FUNCTION: Degrades short-lived regulacory and abnormal proteins in

CC -: FUNCTION: Degrades short-lived regulacory and abnormal proteins in

CC -: CATALITIC ACTIVITY: Hydrolyzes two ATPS for each peptide bond cleaved

CC -: CATALITIC ACTIVITY: Hydrolysis of large proteins such as globin,

CC -: SUBGNIT: Homotetramer (By similarity).

CC -: SUBGNIT: Homotetramer (By similarity).

CC -: SUBCNILULAR LOCATION: Cytoplasmic (By similarity).

CC -: SIMILARITY: Belongs to peptidase family $16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the FWEL outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRODBJU; SMART; SM01382; AAA; 1.
SMART; SM01382; AAA; 1.
SMART; SM0464; LON; 1.
TIGRFAME; TIGRO0753; JON; 1.
TIGRFAME; PS01046; LON SER; 1.
Hydrolase; Serine profease; ATP-binding; Complete proteome.
367 374 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCB_TaxID=29459,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.9%; Score 92; DB 1; Length 812; 22.0%; Pred. No. 15; ative 44; Mismatches 85; Indels
                                                                                                                                                                                           IS-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
ATP-dependent protease La (EC 3.4.21.53).
LON OR BMEI0876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000528; AAL52057.1; ALT_INIT.
PIR; AF361; AF361.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR0035959; AAA_ATPase centr.
InterPro; IPR001270; Chaprnin_clpA/B.
InterPro; IPR00184; Peptidase_S16.
InterPro; IPR008268; Peptidase_S16.
InterPro; IPR008268; Pept_S16_C.
InterPro; IPR008481; Pept_S16_C.
InterPro; IPR008481; Pept_S16_C.
InterPro; IPR008111; Pept_S16_N.
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Pfam; PF02190; LON; 1.
Pfam; PF05362; LON C.
PRINTS; PR0300; CLPPROTEASEA.
PRINTS; PR00830; ENDOLAPTASE.
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                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                      Brucella melitensis.
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                                                                                                                                  LON BRUME
QBYHC6;
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                                                                                   RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 VPSYSFKQFLHPGAASININKSIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 RIMLTFLEFY-----STLLHFVLYKLY------TDSGLIYPPKLDLKKDKIIS- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 RIHYGKFVAEVKFRDAPQDYEPL-----IRAKDKEGLMKLLTF-----TSVEETVR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 --GLSSYILESRQEDSILKLDPTEIEEDVKVESLDASTLKSALNADEANTDETEKEBEGE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 AKRLEENRDS---YTLDHIIKERYPSFPDAIRDIDDALNMLFLFSNLPSTNOVSSKIIND 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 KRVEK-KAVVFGQEVNLNSDDNDNBNR-----KFDPSVASSLYKNWVIPLTKEVQVE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AKAAEQSPDSGNVYTLASVRE-----DLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 IQGFCGSLVEFVVKN-------TEAIQAKAGRYKNPEENAFFPENLPPSI-- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLED COLL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
131001C956787BES CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: May function both in ribosome synthesis and in cell-
                                                                                                                                                                                                                                                                     MEDLINE=22016919; PubMed=12022229;
Oeffinger M., Lueng A., Lamond A., Tollervey D.;
Yeast Pescadillo is required for multiple activities during 608
ribosomal subunit synthesis.";
RNA 8:626-636(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, Z72888; CAA97106.1; -. Germent, Z72888; CAA97106.1; -. Germentine; 141415; -. Germentine; 141415; -. Germentine; 141415; -. Germentine; 141415; -. Germentine; 141415; -. Germentine; 141415; -. Germentine; 181413. Germentine; TRP13. Germentine; TRP13. Germentine; TRP004273; Prinbosomal large subunit biogenesis; IDA. InterPro; IPR00135; BRCT. INTERPROSTITE; PSG9172; BRCT; 1. PROSTITE; PSG9172; BRCT; 1. Ribosome biogenesis; Nuclear protein; Colled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%; Score 92; DB 1; Length 605; 0.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Mismatches 116; Indels
                       SEQUENCE FROM N.A. Wedler E., Wambutt R.; Wedler H., Scharfe M., Wedler E., Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               SEQUENCE OF 1-19 FROM N.A. Hernandez K., Weber N., Wipfli P., Schmidheini T.; Submitted (MAX-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Coiled coil. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                     cycle regulation.
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- SIMILARITY: Contains 1 BRCT domain.
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                                                                                                                                                                                                                                                SUBCELLULAR LOCATION, AND FUNCTION.
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580
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515
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526
560
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14;

Gaps

94;

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STRAIN=1330 / Biovar 1;

WEDLINE=2247741; PubMed=12271122;

REDLINE=2247741; PubMed=12271122;

Read T.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Baugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

A Nelson W.C., Ayodeli B., Kraul M., Shetty J., Malek J., Van Aken S.B.,

A Nelson W.C., Ayodeli B., Kraul M., Shetty J., Malek J., Van Aken S.B.,

A Nelson W.C., Ayodeli B., Kraul M., Shetty J., Malek J., Van Aken S.B.,

A Nelson W.C., Ayodeli B., Kraul M., Shetty J., Malek J., Van Aken S.B.,

A Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,

The Brucella suis genome reveals fundamental similarities between

A Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,

The Brucella suis genome reveals fundamental similarities between

B Froc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

I FUNTION: Degrades short-lived regulatory and abnormal proteins in

D Froc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

I FUNTION: Degrades short-lived regulatory and abnormal proteins in

D Froc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

I FUNTION: Degrades short-lived regulatory and abnormal proteins in

C CATALYTIC ACTIVITY: Hydrolyzes two AIPs for each peptide bond cleaved

In the protein substrate (By similarity).

C CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin,

C SUBGELULAR LOCATION: Cytoplasmic (By similarity).

C SUBGELULAR LOCATION: Cytoplasmic (By similarity).
                                   56 QGFCGSLVEFVVKNTBAIQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASIN 115
                                                                                                                                                                          126 ------AALQ-----BPEBDAVEIEALARSVVS--DFENY-----VK 154
                                                                                                                                                                                                                                       116 INKSIWRMYFKELLPLLATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQ 175
                                                                                                                                                                                                                                                                                                                                                             176 DYEPLIRAKDKEGLMKLLIF-----TSVEETVRKRVEKKAVVFGQEVNLM----- 220
                                                                                                                                                                                                                                                                                                                                                                                                       191 KQEMLSVLSVRERLEKALSFWEAEISVLQVEKRIRSRVKRQMEKTQREYYLNEQMKAIQK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          ---KIPE 190
AAEQSPDSGNVY---TLASVREDLVRQEDTIIYGLIE---RAKFP--SNSHTYDEKYAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 ----SDDNDNENRKFDPSVASSLYKNWVIPLTKEVQVEYL--LRRL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ELGDSEDGRDEVAEIEERITKT-----KLSKEAREKALAELKKL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                155 LNKKI----SPEVVGTASQIDDYSKLADTVASHLAI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-WAR-2004 (Rel. 43, Last sequence update)
ATP-dependent protease La (EC 3.4.21.53).
LON OR BR1106.
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InterPro; IPR003959; AAA ATPase_centr.
InterPro; IPR001970; Chaprin clpA/B.
InterPro; IPR001984; Peptidase_S16.
InterPro; IPR008268; Peptid S16_AS.
InterPro; IPR008269; Peptid S16_C.
InterPro; IPR004815; Pept_S16_C.
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15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last anno
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NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 QGFCGSLVEFVVKNTEALQAKAGRYKNPEENAFFPENLPPSIVPSYSFKQFLHPGAASIN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 INKSIWKMYFKELLPILATSGDDGNYAQTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 LNKKI----SPEVVGAASQIDDYSKLADTVASHLAI-------KIPE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 DYEPLIRAKDKEGLMKLLTF-----TSVEETVRKRVEKKAVVFGQEVNLN----- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AAEQSPDSGNVY---TLASVREDLVRQEDTIIYGLIE---RAKFP--SNSHTYDEKYAQI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22084549; PubMed=12089438;
Tamms I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clark M.A., Baumann P.;
"The (Firo) ATP synthase of Buchnera aphidicola (endosymbiont of
aphids): genetic analysis of the putative ATP operon.";
curr. Microbiol. 35:84-89(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98184963; PubMed=9516544; Clark M.A., Baumann L., Baumann P.; Sequence analysis of a 34.7-kb DNA segment from the genome of Buchnera aphidicola (endosymbiont of aphids) containing grobL, the atp operon, gidA, and rho."; Curr. Microbiol. 36:158-163(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 ----SDDNDNENRKFDPSVASSLYKNWVIPLTKEVQVEYL--LRRL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 92; DB 1; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Indels
                                                                                                                                                                                                                                                                                                                                                                                0F0AC318C9227FBF CRC64;
InterPro; IPR003111; Pept_S16_N.
Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; 1.
Pfam; PF03262; LON; 1.
PRINTS; PF03362; LON; 2.
PRINTS; PR00330; CÎPPROTEASEA.
PRINTS; PR00330; ENDOLAPTASE.
SWART; SW00464; LON; 1.
IGRRAMS; TIGR00763; lon; 1.
PROSITE; PS01046; LON SER; 1.
PYGTOLASE, SETING PIOLEABER; ATP-binding; Compley Death Complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity of the complexity
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
ATPA OR BUSGOO6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 22.0%; Pred. No. 15; 63; Conservative 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                          812 AA; 89794 MW;
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051874;
                                                                                                                                                                                                                                                                                                                                              ACT SITE
SEQUENCE
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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 ----PPSIVPSYSFKQFLHPGA-ASININK-----SIWKMYFKELLPLLATSGDDGNY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 SITDGQIFLESNLFNSGIRPAVNAGISVSRVGSAAQTKIIKKLSSGIRTALAQYHELAAF 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 AÇTAANDLSLLQSISRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLM-----KLLTF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SÓFÀSD---LDÓTTRKOLIYGÓKITELL---KQKOYRPM--SISEQGLMFFIAENNFLDD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 LIERAKFPSNSHTYDEKYAQIQGFCGSLVEFVVKNTEAIQAKAGRYKNPEENAFFPENL- 93
                                                                                                                                SUBUNIT: F-type Arpases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c. SIMILARITY: Belongs to the Arpase alpha/beta chains family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS00152, ATPASE ALPHA BETA; 1. Hydrogen ion transport; Hydrolase; ATP synthesis, CF(1); ATP-binding; Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Gaps
                                                                               subunit.
-!- CATALYALYALY
H(+)(Out).
                                                          gradient across the membrane. The alpha chain is a regulatory
"50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).
-!- FUNCTION: Produces ATP from ADP in the presence of a proton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 91.5; DB 1; Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 TSVEETVRKRVEKKAVVFG------OEVNLNSDDNDNENRKF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQUIRED FOR ACTIVITY.

A -> R (IN REF. 1 AND 2).

EE2884411AFB5E3A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005294; ATP synthF1 alph.
InterPro; IPR00193; ATP synthF1 alph.
InterPro; IPR00194; ATPsse_a/b_c.
InterPro; IPR00194; ATPsse_a/bcentre.
InterPro; IPR00109; ATPsse_a/bN.
InterPro; IPR000790; ATPsse_a/bN.
InterPro; IPR0009005; R1 ATPsse_a/bN.
Pfam; PF00006; ATP-synt_ab; I.
Pfam; PF02874; ATP-synt_ab; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD001099; ATPase aC; 1.
TIGRFAMS; TIGR00962; atpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF008210; AAC38112.1; -.
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269 269 A
510 AA; 56390 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%;
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373
269
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 FVV----KNTEAIQAKAGRYKNPEEN--AFFPENLPP-------SIVPSYSFKQFL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 FIAIRENMGRERIRSEVLRHOHPGMNFGARLPENITPEFVRDEVAAGRAIIPA----NIN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 HPGAASININKSIWKMYFKELLPLLATSGDDGNYAQTAANDLSLLQSI-SRR----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AEQSPDSGNVYTLASVREDLVRQEDTIIYGLIERAKFPSNSHTYDEKYAQIQGFCGSLVE 64
                                                                                                                                 MEDLINE=2134947; PubMed=11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Fickard D., Wain J.,

Churcher C., Mungall K.L., Benley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chllingouth T., Connerton P.,

Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitchead S., Barrell B.G.;

Whitchead S., Barrell B.G.;

Whitehead S., Parry C.,

Whitehead S., Barrell B.G.;

Mature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Required for the synthesis of the hydromethylpyrimidine (HMP) modety of thiamine (4-amino-2-methyl-5-hydroxymethylpyrimidine) (By similarity).
-!- PATHWAY: Thiamine biosynthesis.
-!- SAMILARITY: Belongs to the thic family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 SEBLDDRSSAYTRERLADDGL--DDLRFTGLLTPKRAKAGKRVTQLHYAR-QGIVTPEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 HPESEPMIIGRNF-----LVKVNANIGNSAVTSSIEEEVEKLVWSTRWGADTVMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 IHYGKFVAEVK----FRDAPQDY--EPLIRAKDK-EGLMKLLIFTSVEETVRKRVEK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 LSTGRYIHETREWILRNSPVPIGTVPIYQALEKVNGIAEDLIWEAFRDTLLEQAEQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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InterPro; IPR002817; Thic.
Probom; PD007048; Thic; 1.
Probom; PD007048; Thic; 1.
TIGREAMS; TIGR00190; thic; 1.
Thiamine biosynthesis; Complete proteome.
SEQUENCE 631 AA; 70802 MW; A323C63038E3FA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.8%; Score 91.5; DB 1;
Best Local Similarity 20.3%; Pred. No. 12;
Matches 48; Conservative 55; Mismatches 84;
                  Enterobacteriaceae; Salmonella.
                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINB=20532503; PubMed=11080156;
Vardy L., Toda T.;
"The fission yeast gamma-tubulin complex is required in G(1) phase and is a component of the spindle assembly checkpoint.";
                                        OUNGQ1, 094366; O9P954;
16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Spindle pole body component alp6 (Altered polarity protein 6).
ALP6 OR SPG428.20C OR SPG920.2.01C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Pungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
                                 832 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                        J. 19:6098-6111 (2000)
                            STANDARD;
                                                                                                                                                                                                                                                    Schizosaccharomyces,
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bipolar spindles.
-!-SUBCELULAR LOCATION: Spindle pole body and the microtubule organizing center (MTOC).
-!-SIMILARITY: Belongs to the GCP family.
-!-CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 1.

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EMBL; AB040811; BAA94097.1; ALT\_FRAME. EMBL; AL133306; CAB62095.1; EMBL; AL034382; CAA22295.1; GeneDB SPombe, SPBC428.20c; -.
InterPro, IPR007259, Spc97 Spc98.
Pfam, PF04130, Spc97 Spc98.

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                                                                                                                                                                                                                                                                       108 HPGAASININKSIWK-MYF--KELLPLLATS------GDDGNYAQTAANDLSLLQSI 155
                                                                                                                                                                                                                                                                                                                                       408 HOGOGDV-----VWKGKYFLDKELIPSFLSEELVDKIFLIGKSLNFARYGCGDFDWAQE- 461
                                                                                                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 ----HYQKLVKKLSYRD-PHSLETVVDKAYTESINHLVYL--MEEVFHLTDHLKAIKKYL 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 VFGQE--VNLNSDDNDNE----NRKFDPSVASSLYKNWVIPLTKEVQVEYLLRRLD 261
                                                                                                                                                                                                                                                                                                                                                                                                           156 SRRIHYGKFVAEVKFRDAPQDYEPLIRAKDKEGLMKLLTFTSVEE----TVRKRVEKKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!-SUBUNT: A downler ring-shaped homohexamer of hslV is capped on each side by a ring-shaped hslV homohexamer (By similarity).
-!-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!-SIMILARITY: Belongs to the clpX chaperone family. HslV subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIATE-2012; PubMed=10683204;
MEDIATE-2012; PubMed=10683204;
MEDIATE-2012; PubMed=10683204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.W., Feltwell T., Holroyd S.,
Jugels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 403:665-668(2000).
-!- FUNCTION: Chaperone subunit of a proteasome-like degradation complex (By similarity).
                                                                                                                                                                                                              37;
                                                                                                                                          DB 1; Length 832;
                                                                                                                                                                                                              Indels
                                       MISSING (IN REF. 2).
C92771C3DBF5C01A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
ATP-dependent hal protease ATP-binding subunit halu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P32168, 1002.
HAWAP; MF 00249; -; I.
InterPro; IPR00359; AAA ATPase.
InterPro; IPR00359; AAA ATPase centr.
InterPro; IPR00491; Hsp_HslVU.
PFam; PF00004; AAA, 1.
TIGRRAMS; TIGR0390; hslU, 1.
Chaperone; ATP-binding; Complete proteome.
NP_BIND
56 63 ATP-binding; Complete proteome.
                                                                                                                                   6.8%; Score 91.5; Dilarity 25.4%; Pred. No. 17; Conservative 28; Mismatches
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                                                                   832 AA; 95996 MW;
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                                       675
Microtubule; Mitosis.
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                                                                                                                                                                   Local Similarity
les 45; Conserv
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Q9PHLO;
                                       CONFLICT
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HSLU CAMUE
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                                  OM protein - nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                                                                                                                                                      Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
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                                                                                                                                                                                                                                                    Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M. Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Yu,H.C., Yu,G., Yuan,S., Bowser,L., Chen,H., Chen,k., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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The RIKEN Genomic Sciences Center (GSC) members carried out the Collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Ramiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K.,
Wu, H.C., Yu, G., Yuan, S., Bowser, L., Carninci, P., Chen, H.,
Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Theologis, A.,
Theologis, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
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13 (botes, D.C., Davis, K.R., Weessner, J.P., Gorlach, J., Hamilton, C.M., Hoffman, N.E., Kloti, A.S., Zayed, A. and Ascenzi, R.A.
15 (Ascenzial and compositions for the modulation of chorismate synthase and chorismate mutase expression or activity in plants
15 (Ascenzial) - Ascenzial 15 (CT-2002;
16 (Ascenzial) - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Ascenzial - Asc
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1 (bases 1 to 1006)

Boyes, D. C., Davis, K.R., Woessner, J.P., Gorlach, J., Hamilton, C.M.,
Hoffman, N.E., Inti, A.S., Zayed, A. and Ascenzi, R.A.
Methods and compositions for the modulation of chorismate synthase
and chorismate mutase expression or activity in plants
Patent: US 6465217-A 3 15-OCT-2002;

Location/Qualifiers
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Mulpuri, R. and Kjentrup, S.
Methods and compositions for the modulation of chorismate synthase and chorismate mutase expression or activity in plants
Patent: WO 0202798-A 3 10-JAN-2002;
Paradigm Genetics Inc. (US)
Location/Qualifiers
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Sequence 3 from Patent W00202798.
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IHYGKRVAEVKRINAPODYEPALIAKOLIFEKVEEMWKKAVQKKAETFGGE
VKFNSGYGDESKKKYKUDPLLASRIYGEWLIPLITKLIVEVEYLLIRELD"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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                                                ProLeulleArgAlaLysAspLysGluGlyLeuMetLysLeuLeuThrPheThrSerVal 198
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                                                                                ccreccarroccecrcacaracacacacrrrcarcaaccrorrcaccrrrraacaaacra
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Patent: WO 0200901-A 3 03-AN-2002;
Sungene GmbH & CO. KgAA (DE)
Location/Qualifiers
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermacophyta; Magnoliophyta; edicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E Bberhard, J., Ehrlar, T.T., Epple, P., Felix, G., Raesecke, H.R., Amrhein, N. and Schmid, J.

Cytosolic and plastidic chorismate mutase isozymes from Arabidopsis thaliana: molecular characterization and enzymatic properties

E Plant J. 10 (5), 815-821 (1996)
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Arabidopsis thaliana chorismate mutase mRNA, complete cds.
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HYYESALHFYRLSWINKIWDIYPFRELLPLFVKRGDGGNYSFYASDLACLQALSRR
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                                        GluGluThrValArgLysArgValGluLysLysAlaValValPheGlyGluGluValAsn 218
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              cerecearrescereagaragasascerrrsargasscrerrsacerrrsasscrars
                                                                                                              SerSerLeuTyrLysAsnTrpVallleProLeuThrLysGluValGlnValGluTyrLeu
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Conservative:
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1 MetAlaLysAlaAlaGluGlnSerProAspSerGly-----AsnValTyrThrLeuAla 18

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Aro65238
Arabidopsis thaliana putative chorismate mutase CM2 (At5g10870)
mRNA, complete cds.
Aro65238
Aro65238
FLI CDNA.
Arof5238 thaliana (thale cress)
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1055)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
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                            39 AlaLysPheProSerAsnSerHisThrTyrAspGluLysTyrAlaGlnIleGlnGlyPhe
                                                                                                                               244 ITCTCTTCTCTCACTGAGTTTTTCGTCAGAGAGAGAAATCATCCAAGCTAAGGTAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 SerValArgGluAspLeuValArgGlnGluAspThrileIleTyrGlyLeuIleGluArg
                                                                                                                                                                                                59 CysGlySerLeuValGluPheValValLysAsnThrGluAlaIleGlnAlaLysAlaGly
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US-10-624-061-16 (1-261) x AY065238
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Yamada, K., Banh, J., Chang, C.H., Chang, E., Dale, J.M., Tang, C.C., Torlunt, M. D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Torlunt, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, E., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinn, P., Southwick, A., Shinn, P., Southwick, A., Shinn, P., Submission Center, 800 Buchanan Submission Center, 800 Buchanan
                                                                                                                                                                                                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chang,C.H., Chang,E., Dalle,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin,Punk,G., Kim,C., Lam,B., Lin,J., Meyers,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative chorismate mutase CM2"
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THYSPSALPHYALSWINKOJNDIYFRELLPLPKVRGDDGONYSPTAASDLACLQALSRR
IHYGKFVAEVKRRDAPQDYEBAIRAQDREALMKLLTERKVERWYKRVQKKAETFGQE
VKFNSGYGDESKKKYKVDPLLASRIYGEWLIPLTKLVEVGYLLRRLD"
                                                                                                                                                                                                                                                                                            Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the Collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Sacou,M., Kamiya,A., Sakural,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakurai, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada, K. (SSP/PGEC) and Seki, M. (RIXEN GSC) contributed equally to this work. Shinozaki, K. (RIXEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ecotype="Columbia"
/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/XhoI insert."
Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K. Bovis, R. W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones
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/organia="Arabidopsis thaliana"
|mol_type="mRNA"
|db_xref="taxon:3702"
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/clone="RAFL09-41-E09 (R18739)"
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/gene="At5g10870"
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/note="compared to
/replace="t"
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843 GATTGGATCATGCCTTTAACAAAAGAGGTTCAAGTGGAGTACTTGCTCAGAAGACTGGAC 1002
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883 GAAGGGAATGAATCTCATGTTTACAAAICAGTCCGATCTTAGTIGGTGACTTATAGA
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same, and methods of use
Patent: WO 0216655-A 737 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations
(CH)
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Mismatches:
Indels:
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1. .1005
/ Organism="Arabidopsis thaliana"
/ hol_type="unassigned DNA"
/ db_xref="taxon:3702"
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Matches:
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 TCATTGGTGGAATTTGTTGTTAAGAATACAGAGGCCATTCAAGCTAAGGCTGGAAGATAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysAsnProGluGluAsnAlaPhePheProGluAsnLeuProProSerIleValProSer 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 TACTCCTTCAAACAGTTTTTGCATCCTGGTGCTGCTTCAATTAACATAAACAAGTCATCT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgGluAspLeuValArgGlnGluAspThrIleIleTyrGlyLeuIleGluArgAlaLys
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Matches:
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                   Unknow...
Unclassified.
1 (bases 1 to 525)
Falco,S.C., Famodu,O.O. and Lee,J.-M.
Aromatic amino acid biosynthetic enzyme
Patent: US 6627798-A 5 30-SEP-2003;
Location/Qualifiers
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Sequence 737 from Patent WO0216655.
AX506042
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    525
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462 109 522 129 582 149 642 169 702 189 762 209 822 229 882 241 942 261

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Unknown.
Unknown.
Unclassified.
Unclassified.
L (bases I to 1207)

Boyes, D.C., Davis, K.R., Woessner, J.P., Gorlach, J., Hamilton, C., Davis, K.R., Zayed, A. and Ascenzi, R.A.
Hoffman, N.E., Kloti, A.S., Zayed, A. and Ascenzi, R.A.
Methods and compositions for the modulation of chorismate synthase and chorismate mutase expression or activity in plants
Patent: US 6465217-A 8 15-OCT-2002;
Location/Qualifiers
ProGluAsnLeuProProSerIleValProSerTyrSerPheLysGlnPheLeuHisPro 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 GlyalaalaSerileAsnIleAsnLysSerileTrpLysMetTyrPheLysGluLeuLeu 129
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                                     242 AsnTrpValileProLeuThrLysGluValGluValGluTyrLeuLeuArgArgLeuAsp
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US 6465217.
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AR236639
AR236639.1 GI:27280725
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Boyes, D.C., Davis, K.R., Woessner, J.P., Gorlach, J., Hamilton, C.M.,

Hoffman, N.E., Kloti, A.S., Zayed, A. and Ascenzi, R.A.

Hoffman, and compositions for the modulation of chorismate synthase
and chorismate mutase expression or activity in plants

Patent: US 6465217-A 2 15-OCT-2002;
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2 from patent US 6465217.
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Search completed: September 25, 2004, 04:17:47 Job time : 4199 secs

Scoring table:

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(LEEJ/) LEE J.
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-MODEL=frame+ p2n.model.-DEV=Xlh
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-Q=/cgn2_1/USPTO_spool/US10624061/runat_BNFTX=rsng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UMTTS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=Ept -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO MAAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV TINROUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1 MAKAAEQSPDSGNVYTLASV......NWVIPLTKEVQVEYLLRRLD
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                          nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                           3373863 seqs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
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Score

Result No No us-10-624-061-16.rng

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The invention discloses isolated polymucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of animals. In the aromatic amino acid biosynthatic pathway chorismate is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for trynssine and phenylalanine to biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymelic enzyme polypeptide in a host cell, obtaining a nucleic acid is polymucleotide that affects the level of expression of a tyrosine polypeptide and regardating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used good attibodies. Chorismate mutase and prephenate dehydrogenase are good trynsles enzymes may be used to increase the content of aromatic amino of these enzymes may be used to increase the content of aromatic amino of these enzymes may be used to increase the content of aromatic amino of inhibitors of those enzymes that may be used as herbicides. The content cand physical mapping of the genes and as markers for traits mutase on the service of the genetic and physical mapping of the genes and as markers for traits mutase on the content cands and as markers for the mates of the content cands and as markers for the mates of the content cands and as markers for the cands of the content cands and as markers for the cands of the content cands and as markers for the cands of the content cands and as markers for the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the cands of the c
                                                                                                                                                                                                        New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids; useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 22; 32pp; English.
                                  Lee J;
                              Famodu 00,
                                                                                                  WPI; 2003-328651/31.
P-PSDB; ABU08094.
                              Falco SC,
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Sequence 1020 BP; 322 A; 176 C; 223 G; 299 T; 0 U; 0 Other;

<del>-</del>	383 IGGAAAATGTATTTCAAAGAGTTACTTCCATTGCTTGCTACTTCGGGTGATGATGGCAAC 442
ð.	141 TyrAlaGlnThrAlaAlaAsnAspLeuSerLeuLeuGlnSerIleSerArgArgIleHis 160
<b>q</b> Ω	443 TATGCGCAAACTGCAGCTAATGACCTTTCATTATTGCAGTCCATCTCTAGAAGGATTCAC 502
ð	161 TyrGlyLysPheValAlaGluValLysPheArgAspAlaProGlnAspTyrGluProLeu 180
<b>Q</b> C	503 TATGGAAAGTTTGTAGCTGAGGTGAAATTCAGGGATGCTCCTCAAGACTACGAGCCTTTA 562
<i>ò</i> €	181 IleArgAlaLysAspLysGluGlyLeuMetLysLeuLeuThrPheThrSerValGluGlu 200 
ò	01 ThrValArgLysArgValGluLysLysAlaValValPheGlyGlnGluValAsnLeuAsn 22
qq	623 ACGGTGAGGAAGAGAGTTGAAAAAAAGGCTGTGGTGTTTGGGCAGGAAGTAGAATCTTAAC 682
ò	221 SerAspAspAspAsnGluAsnArgLysPheAspProSerValAlaSerSerLeuTyr 240
qa	GACAATGAAAACCGTAAATTGATCCATCAGGGCTTCTAGCT
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q	cicicaccaaddagricaddricadraccicridcgc
δy	261 Asp 261
đ	803 GAC 805
REST ABZ1 ID	SULT 2 213167 AB213167 standard; DNA; 798 BP.
¥8;	ABZ13167;
첫 E :	21-JAN-2003 (first entry)
OE	Arabidopsis thaliana stress regulated gene SEQ ID NO 972.
₹₹\$	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
88	Arabidopsis thaliana.
Y N.S	WO200216655-A2.
<b>₹</b> ₽\$	28-FEB-2002.
4 E	24-AUG-2001; 2001WO-US026685.
44 44 44 44 44 44	24-AUG-2000; 2000US-0227866P. 26-JAN-2001; 2001US-0264647P. 22-JUN-2001; 2001US-0300111P.
XX PA	(SCRI ) SCRIPPS RES INST. (SYGN ) SYNGENTA PARTICIPATIONS AG.
XZ	Harper JF, Kreps J, Wang X, Zhu T;
<b>≾</b> ≝\$	WPI; 2002-304127/34.
E E E	Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
X S. X	Claim 144; SEQ ID NO 972; 577pp + Sequence Listing; English.
<b>188</b>	The invention relates to identifying a stress condition to which a plant
888	representative of expressed polymorlectides in array or probes representative of the plant cel
888	detecting a profile of expressed polynuclectides in the plant cell characteristic of a stress response. The method is useful in the characteristic of a stress response.
כר	production of transgenic plants, cells and seed

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with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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This invention describes a novel method for the preparation of fine chemicals by culturing organisms in which the shikimate pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutase and/or prephenate dehydrogenase, linked to at least one regulatory sequence for transcription or translation in plants. The method is used to produce chemicals, particularly Vitamins B or K and/or ubiquinone, useful e.g. as fat-soluble antioxidants (in feeds, pharmaceuticals and cosmetics), but also aromatic amino acids, salicylic or folic acid derivatives, phenylpropanoids, flavanoids etc., especially in transgenic plants. Also plants with increased Vitamin B contents have improved resistance to abiotic stress, e.g. frost and drought. Transgenic plants with an altered abiotic stress, e.g. frost and drought. Transgenic plants with an altered chicking processed foodstuffs. Transgenic plants with modified shikimate pathways have increased content of desired chemicals, particularly tocopherols and/or tocotrienols. This sequence encodes the construct pCR-Script/AtCM-ITP-ATCM-2 which is composed of the Arabidopsis thaliana plastid chorismate mutase-1 transit peptide and a Arabidopsis thaliana chorismate mutase-1 transit peptide and a Arabidopsis thaliana chorismate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparing fine chemicals, particularly Vitamins E and K, useful as anticxidants e.g. in foods or medicine, by growing organisms with altered shikimate biosynthesis pathway.
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                                                                                                                                       Construct pCR-script/AtCM-1TP-AtCM2
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21-DEC-2000; 2000DE-01064454.
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This invention describes a novel method for the preparation of fine chemicals by culturing organisms in which the shikimate pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutase and/or translation or translation in plants. The method is used to produce translation or translation in plants. The method is used to produce chemicals, particularly Vitamins E or K and/or ubiquinone, useful e.g. as aromatic anino acide, salicylic or folic acid derivatives, pherypropanoids, flavanoids etc., especially in transganic plants. Also plants with increased Vitamin E contents have improved resistance to blants with increased Vitamin E contents have improved resistance to blants with increased Vitamin E contents have improved resistance to blants with increased foodstuffs. Transgenic plants with an altered shikimate pathway are useful as foods, fodder and in preparation of processed foodstuffs. Transgenic plants with modified shikimate pathways and/or tocotrienols. This sequence encodes the Arabidopsis thallana and/or tocotrienols. This sequence encodes the Arabidopsis thallana cytosolic chorismate mutase-2 protein used in the method of the invention
                                                                                                                                                                                                                                           Preparing fine chemicals, particularly Vitamins E and K, useful as antioxidants e.g. in foods or medicine, by growing organisms with altered shikimate biosynthesis pathway.
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(SUNG-) SUNGENE GMBH & CO KGAA.
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72.83%
61.13%
61.09%
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The present sequence is that of an antisense oligonucleotide that is specific for Arabidopsis thaliana chorismate-mutase-2 (CM) mRNA. CM catalyyses the conversion of chorismate to prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine biosynthesis. It is essential for plant growth, inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense and sense polynucleotides, double-stranded RNA and ribozymes, and related expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that
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and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
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                                                                                                                                                                                                                                                                                                                                                            244 TICICITCICACAGAGITITICGICAGAGAGACAGAAATCAICCAGAGCIAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 ATTCACTACGGTAAATTTGTAGCTGAGGTCAAATTCAGAGATGCTCCACAAGATTACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCGCATCTACGGGGAATGGCTTATCCCTCTCACTAAGCTCGTTGAGGTTGAGTATCTT
                                                                                                                                                                                  ServalArgGluAspLeuValArgGlnGluAspThrIleIleTyrGlyLeuIleGluArg
                                                                                                                                                                                                                                                                                                                                 CysGlySerLeuValGluPheValValLysAsnThrGluAlaIleGlnAlaLysAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                       ArgTyrLysAsnProGluGluAsnAlaPheProGluAsnLeuProProSerIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                          304 AGATATGAATACCCGGAAGAGAATCCTTTCTTCCTTCAGAACATTCCTCACTCGGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerileTrpLysMetTyrPheLysGluLeuLeuProLeuLeuAlaThrSerGlyAspAsp
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 Mismatches:
               Indels:
                                   Gaps:
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                                                                        US-10-624-061-16 (1-261) x ABA91394
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61.09%
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 Best Local Similarity:
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               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a full-length cDNA encoding Arabidopsis that chalana chorismate mutase-2 (CM), an enzyme that catalyses the conversion of chorismate to prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine biosynthesis. CM is essential for plant growth; inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and development abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense (see ABA91400) and sense polymucleotides, double-stranded RNA and ribozymes, and related expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for sense is also a target for the identification of herbicides, and methods are provided for using CM in the identification of herbicide candidates. Methods are also provided for identifying compounds that stimulate the expression or function of CM. These can be used to promote growth and
                   236
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                                                    224
                                                                                                             ---AspProSerValAla
                                           SerSerLeuTyrLysAsnTrpValIleProLeuThrLysGluValGlnValGluTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds useful for modulating and inhibiting plant groand development, by using chorismate synthase and chorismate mutase targets which are essential for plant growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamilton CM;
Allen K, Mulpuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 226 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Chorismate mutase-2; herbicide; plant; enzyme; gene;
                   LeuAsnSerAspAspAsnAspAsnGluAsnArgLysPhe--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
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Zayed A, Ascenzi RA,
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis chorismate mutase-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 64-65; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woessner JP,
                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                              ABA91394 standard; cDNA; 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PARA-) PARADIGM GENETICS INC
                                                                                                                                                                                        CTACGTCGTCTCGAT 149
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                                                                                                                                                                    LeuArgArgLeuAsp 261
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818.00
72.83%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-154754/20.
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Hoffman NE,
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Score:
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118

423 138 483 158 543 178 603 198 663

363

9

243

S S

38

303

78

236

783 256 843 Soybean; plant; gene; ss; chorismate mutase; expressed sequence tag; EST;

Percent Similarity:

chorismate; anthranilate;

/partial /note= "No start or stop codon shown"

"Chorismate mutase"

/\*tag= a /product= . .438

Location/Qualifiers

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New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
      tryptophan, prephenate, tyrosine, phenylalanine, prephenate dehydrogenase, herbicide, food crop.
acid; diet; biosynthesis;
                                                                                                                                                                                                                                               Claim 3; Page 16; 32pp; English.
                                                                                                                    99US-00454279.
                                                                                                                                  98US-0110845P
                                                                                                                                                                           SC, Famodu 00,
                                                                                                                                                                                         2003-328651/31.
                                                                                                                                               (FALC/) FALCO S C.
(FAMO/) FAMODU O O.
(LEEJ/) LEE J.
                                                                                                                                                                                                P-PSDB; ABU08089
                                                                                         US2002184658-A1
 amino
                                                                                                                     03-DEC-1999;
                                                                                                                                  04-DEC-1998;
                                                                                                       05-DEC-2002
                            Glycine max
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The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets of animals. In the aromatic amino acid biosynthesic polymented to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyzosine and phenylalanine to prephenate. Also disclosed are methods for selecting an isolated polymucleotide that affects the level of expression of a tyrosine polymetric enzyme polypeptide in a host cell, obtaining a mucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of those enzymes may be used to increase the content of aromatic amino of these enzymes may be used to increase the content of aromatic amino of these caps. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used as herbicides. The mutase content cand physical mapping of the genes amazers for trains to those genes. The sequence presented is a soybean chorismate mutase expressed sequence tag (BST)

Sequence 525 BP; 160 A; 103 C; 111 G; 148 T; 0 U; 3 Other;

gnment Scores:

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Conservative:
Mismatches:
Indels:
 Length:
Matches:
                                                                                 US-10-624-061-16 (1-261) x ABX93053 (1-525)
2.72e-81
767.50
95.29%
95.29%
57.32%
                         Percent Similarity:
Best Local Similarity:
                                              Query Match:
DB:
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1 MetalalysalaalagluglnSerProAspSerGlyAsnValTyrThrLeuAlaSerVal

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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                   TyrAlaGln-ThrAlaAlaAsnAspLeuSerLeuLeuGlnSerIleSerArgArgIleHi 160
                                                                                                                                                            255
                                                                                                                                                                                                                  315
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                                                                                                                                                                                                                                           TyrSerPheLysGlnPheLeuHisProGlyAlaAlaSerIleAsnIleAsnLysSerIle 120
                                                                                                                                                                                                                                                                     316 racrectreaaacagritritgearecregrecrectrearraacaraabacaagrearer 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an
                                                LysAsnProGluGluAsnAlaPhePheProGluAsnLeuProProSerIleValProSer 100
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                                                                                                                                                                                                                                                                                                                                                                             436 TATGCGCAAAACTGCAGCTAATGACCT-TCATTATTGCAGTC-ATCTCTAGAAGGAT-CA
                                                                                                                                                                                                                                                                                                121 TrpLysMetTyrPheLysGluLeuLeuProLeuLeuAlaThrSerGlyAspAspGlyAsn
                                                                                                                                                     256 AAAACCCTGAAAAACGCCTTCTTCCCAGAAAATTTACCACCATCAATTGTGCCATCT
16 ATGGCCAAAGCAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGTG
                                                                             41 PheProSerAsnSerHisThrTyrAspGluLysTyrAlaGlnIleGlnGlyPheCysGly
                                                                                                                                  SerLeuvalGluPhevalvalLysAsnThrGluAlaIleGlnAlaLysAlaGlyArgTyr
                            21 ArgGluAspLeuValArgGlnGluAspThrileIleTyrGlyLeuIleGluArgAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana stress regulated gene SEQ ID NO 737.
                                                                                                                                                                                                                                                                                                                                                                                                           sTyrGlyLysPheValAlaGluValLys 169
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ12932 standard; DNA; 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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RESULT

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array or probes representative of the plant cell genome, and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                    AspSerGlyAsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGlnGluAsp
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1005 BP; 287 A; 205 C; 235 G; 278 T; 0 U; 0 Other;
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46
75
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Matches:
Conservative:
Mismatches:
Indels:
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                                           1.17e-72
698.00
68.08%
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                                                                                           Local Similarity:
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                                                                                                        Query Match:
DB:
                                              No.:
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The present sequence is that of a full-length cDNA encoding Arabidopsis thaliana chorismate mutase-1 (CM), an enzyme that catalyses the conversion of chorismate to prephenate in a branch of the shikinate pathway leading to phenylalanine and tyrosine biosynthesis. CM is essential for plant growth; inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense (see ABA91399) and sense polynucleotides, double-stranded PNA and ribozymes, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ટ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that produce seedless fruit. C is also a target for the identification of herbicides, and methods are provided for using CM in the identification of herbicide candidates. Methods are also provided for identification compounds that stimulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to promote growth and
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                                                                                                                                                                                                                                                                                                                                                                                                CM;
Mulpuri I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other;
                                                                                                                                                                                                                                                                                                                                                                                              pessner JP, Gorlach J, Hamilton
Zayed A, Ascenzi RA, Allen K,
                                                                                                                                                      Chorismate mutase-1; herbicide; plant; enzyme; gene; ss
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-624-061-16 (1-261) x ABA91393 (1-1207)
                                                                                                                   Arabidopsis chorismate mutase-1 cDNA
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                BP
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                CDNA; 1207
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                                                                                                                                                                                                                                                                                                                           05-JUL-2000; 2000US-00610040.
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696.00
68.08%
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Kloti AS,
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                ABA91393 standard;
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ThrieleTyrGlyLeulleGluargalaLysPheProSerAsnSerHisThyrAsp

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295 AGCATTATATTTGGGCTATTGGAGAGAGCCAAGTACTGTTACAATGCTGATACTTATGAT 354
                                             ProGluAsnLeuProProSerIleValProSerTyrSerPheLysGlnPheLeuHisPro 109
                                                                                                                                                             CTGATGATCTACCAGAGCCTATGTTCCCTCTTCAGTACCCAAAGGTGTTGCATTT 534
                                                                                                                                                                                                    110 GlyAlaAlaSerIleAsnIleAsnLysSerIleTrpLysMetTyrPheLysGluLeuLeu 129
                                                                                                                                                                                                                       ProLeuLeuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeu 149
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|TGGATATGCTGACATTCCCGACTGTGGAAGATGCGATAAAGAAGAGAGTTGAGATGAAA 834
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                                                                                  ThrGluAlaileGlnAlaLysAlaGlyArgTyrLysAsnProGluGluAsnAlaPhePhe 89
                            50 GluLysTyrAlaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsn
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Zayed A, Ascenzi RA, Allen K, Mulpuri R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis chorismate mutase-1 antisense polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chorismate mutase-1; enzyme; plant; antisense; ss.
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Kloti AS,
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Hoffman NE,
Kjemtrup S;
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GATGAGAGTGAGAGTTTGACTCTTGAAGGTATTAGAAACTCTTTGATCCGTCAAGAGGAC 914

10 AspSerGlyAsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGlnGluAsp

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30 ThrileileTyrGlyLeuIleGluArgAlaLysPheProSerAsnSerHisThrTyrAsp GluLysTyrAlaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsn 

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ProGluAsnLeuProProSerIleValProSerTyrSerPheLysGlnPheLeuHisPro 109

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GlyAlaAlaSerileAsnileAsniysSerileTrpLysMetTyrPheLysGluLeuLeu 673 GCTGCTGATTCGATAAACATAAACAAGAAGATATGGAACATGTACTTCAGAGACCTTGTT ProleuleuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeu

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150 SerLeuLeuGinSerIleSerArgArgIleHisTyrGlyLysPheValAlaGluValLys 553 ATCTGCCTTCAGTGTCTCTCAAAGAGAATCCATTACGGTAAATTTGTTGCAGAAGCTAAA PheArgAspAlaProGlnAspTyrGluProLeuIleArgAlaLysAspLysGluGlyLeu

ACTGAGAAGCTTCACGCTAAGGTTGGTAGGTTTAAGAGTCCTGATGAACATCCTTTCTTC

ThrGluAlaIleGlnAlaLysAlaGlyArgTyrLysAsnProGluGluAsnAlaPhePhe

MethysleuleuThrPheThrSerValGluGluThrValArgLysArgValGluLysLys 209 

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specific for Arabidopsis that an anticonstruction of the catalyses the conversion of chorismate prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine biosynthesis. It is essential for plant growth, inhibition of CM gene expression in plant shedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense and sense polynucleotides vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that produce seedless fruit
                                                                 Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
                                                                                                                                                                                                                 The present sequence is that of an antisense oligonucleotide that
                                                                                                                                                                  Claim 35; Page 71; 73pp; English.
                       WPI; 2002-154754/20.
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Sequence 1207 BP; 354 A; 278 C; 232 G; 343 T; 0 U; 0 Other;

.61e-72 696.00 68.08% 50.38% 51.98%

Alignment Scores:

Percent Similarity: Best Local Similarity:

Query Match: DB:

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Conservative: Mismatches: Indels: Length: Matches:

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      210 AlaValValPheGlyGluValAsnLeuAsnSerAspAspAsnAspAsnGluAsnArg 229
                                                                                                 261
                                                                                                                                                                                                                                                         Rice; plant, gene, ss, chorismate mutase, aromatic amino acid, diet, biosynthesis, chorismate, anthranilate, tryptophan, prephenate; tyrosine, phenylalanine; prephenate dehydrogenase; herbicide; food crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acid biosynthetic pathway chorismate is converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymoclocide that affects the level of expression of a tyrosine biosynthetic enzyme polypeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good
                                                      241
                                                                           254
                                                                                                                        194
                     313 GAAGGGAATGAATCTCATGTTTACAAATCAGTCCGATCTTAGTTGGTGACTTATATGGA
                                                                                                             --LysPheAspProSerValAlaSerSerLeuTyrLys
                                                                                             AsnTrpValIleProLeuThrLysGluValGlnValGluTyrLeuLeuArgArgLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
                                                                                                                                                                                                                                                                                                                                                                "Chorismate mutase"
                                                                                                                                                                                                                                                                                                                                                                                        note= "No start codon shown"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
253. .1026
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P-PSDB; ABU08093.
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(FAMO/) FAMODU O O.
(LEEJ/) LEE J.
                                                                                                                                                                   ABX93057 standard;
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                                                                                                                                                                                                                                                                                                        Oryza sativa
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targets for herbicides that will not affect animals, and overexpression of these anizymes may be used to increase the content of aromatic amino acid in food crops. The polypeptides may also be used to design and/or identify inhibitors of those enzymes that may be used as herbicides. The muclaic acids may be used or create transgenic plants, as probes for the genetic and physical mapping of the genes and as markers for traits inked to those genes. The sequence presented is a rice chorismate mutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetAlaLysAlaAlaGluGlnSerProAspSerGlyAsnValTyrThrLeuAlaSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ArgGluAspleuValArgGlnGluAspThrileIleTyrGlyLeuIleGluArgAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CICCAGIAICCAAAGGITITIGCAICCTAITIGCIGAITCTAITAAIAICAACAAGGAGAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerieuvalGluPheValValLysAsnThrGluAlaIleGlnAlaLysAlaGlyArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 TCTTTGGTTGATTCATGGTTAGAGAAACCGAAAAACTACATCAACAGGTTGGGAGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 TyrSerPheLysGlnPheLeuHisProGlyAlaAlaSerIleAsnIleAsnLysSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyralaGlnThralaalaasnaspLeuSerLeuLeuGlnSerIleSerargarglleHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 GCTATIGAACATAGGGTGGAAGCTAAGGCTAAGGATCTTTGGACAGGTGGATTTAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAGCTACAGGATCATGCCGCTAACCAAGGAGGTTCAAGTAGCCTACTTGCTGAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGGATCCAGTGCTCTTTGTGACACGATCTGCTTGCAGGCGCTCTCCAAAAGAATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspAspAspAspAspAspanGluAspArg---LysPheAspProSerValAlaSerSerLeu
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81
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Mismatches:
Indels:
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Matches:
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685.50
68.70%
51.53%
51.19%
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Best Local Similarity:
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02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
04-AUG-1999;
04-AUG-1999;
   Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                   Arabidopsis thaliana DNA fragment SEQ ID NO: 2614.
                                                                                               AAC33324 standard; DNA; 1274 BP
                                                                                                                                                                                                                                                                                                                                                                                                 99US-0121825P.
99US-0121848P.
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                                                                                                                                                          17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                      1018 TTGGAT 1023
           260 LeuAsp 261
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
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969 GAAGGGAATGAATCTCATGTTTACAAATCAGTCCGAT-CTTAGTTGTGACTTATATGGA 1027
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                                         428
                                                                              488
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                                                                                                                                  109
                                                                                                                                                    608
                                                                                                                                                                                       668
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                                                                                                                                                                                                      130 ProLeuleuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeu 149
                                                                                                                                                                                                                         728
                                                                                                                                                                                                                                                                            PheArgAspAlaProGlnAspTyrGluProLeuIleArgAlaLysAspLysGluGlyLeu 189
                                                                                                                                                                                                                                                                                        49
                                                                                                                                                                                                                                                           729 ATCTGCCTTCAGGTCTCTCAAAGAGAATCCATTACGGTAATTTGTTGCAGAAGCTAAA 788
                                                                                                                                                                                                                                                                                                                           69
                                                                                               89
                                                                                                                                                                                                                                                                                                                                                   210 AlaValValPheGlyGluValAsnLeuAsnSerAspAspAsnAspAsnGluAsnArg 229
                                                                                                                                                                                                                                                                                                                                                                                       Corn; plant; gene; ss; chorismate mutase; aromatic amino acid; diet; biosynthesis; chorismate; anthranilate; tryptophan; prephenate; tyrosine; phenylalanine; prephenate dehydrogenase; herbicide; food crop.
                                                                    30 ThrilelleTyrGlyLeuileGluArgAlaLysPheProSerAsnSerHisThrTyrAsp
                               50 GluLysTyrAlaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsn
                                                                                           ThrGluAlaIleGlnAlaLysAlaGlyArgTyrLysAsnProGluGluAsnAlaPhePhe
                                                                                                         ProGluAsnLeuProProSer11eValProSerTyrSerPheLysGlnPheLeuHisPro
                                                                                                                                          110 GlyAlaAlaSerileAsnileAsniysSerileTrpLysMetTyrPheLysGluLeuLeu
                                                                                                                                                                                 609 GCTGCTGATTCGATAAACATAAACAAGAAGATATGGAACATGTACTTCAGAGACCTTGTT
                                                                                                                                                                                                                        909 ACCCGAACATACGGGCAAGAAGTGAAAGTTGGGATGGAGGAGAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                 WetLysLeuLeuThrPheThrSerValGluGluThrValArgLysArgValGluLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                        242 AsnīrpValIleProteuThrLysGluValGlnValGluTyrLeuLeuArgArgLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
3...998
/*teg= a 'Thorismate mutase' 'product= "Chorismate mutase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX93056 standard; cDNA; 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn chorismate mutase cDNA,
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9905-0149422P.
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9905-0149930P.
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9905-0151066P.
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99US-0161993P.
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Best Local Similarity:
Query Match:
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29-OCT-1999
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US-10-624-061-16 (1-261) x AAC33324 (1-1274)

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596 149 929 189 776

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SerLeuLeuGlnSerlleSerArgArglleHisTyrGlyLysPheValAlaGluValLys 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
                                                                                                                                                          ProLeuLeuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeu
             90 ProGluAsnLeuProProSerIleValProSerTyrSerPheLysGlnPheLeuHisPro
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717 TITCAAGAGTCCCCTGAAGCTIACACGCCAGACCATAATAGCCCAAGACCGTGATCAACTC
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                                                                                    110 GlyAlaAlaSerIleAsnIleAsnLysSerIleTrpLysMetTyrPheLysGluLeuLeu
                                                                                                                        537 ATTGCTGATTCTATCAATATCAACAAGAGATTTTGGAAAATGTATTTTGATGAACTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutase-3; herbicide; plant; enzyme; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  957 AAGGAGGTTGAGGTCGCGTACTTGCTTAAGAGGCTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 LysGluValGlnValGluTyrLeuLeuArgArgLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Woessner JP, Gorlach J,
Zayed A, Ascenzi RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis chorismate mutase-3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 37; Page 65; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA91395 standard; cDNA; 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PARA-) PARADIGM GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35-JUL-2000; 2000US-00610040.
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, Kloti AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
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Hoffman NE,
Kjemtrup S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses isolated polynucleotides encoding chorismate mutase polypeptides. Aromatic amino acids must be included in the diets of animals. In the aromatic amino acids must be included in the diets converted to anthranilate during tryptophan biosynthesis and is converted to prephenate, the branch point for tyrosine and phenylalanine biosynthesis. Chorismate mutase catalyses the conversion of chorismate to prephenate. Also disclosed are methods for selecting an isolated polymenter and affects the level of expression of atyrosine polymeptide in a host cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and a vost cell, obtaining a nucleic acid fragment encoding a tyrosine biosynthetic enzyme polypeptide and evaluating compounds for their ability to inhibit the activity of a tyrosine biosynthetic enzyme. The polypeptides can be used produce antibodies. Chorismate mutase and prephenate dehydrogenase are good targets for herbicides that will not affect animals, and overexpression of those enzymes may be used to increase the content of aromatic amino acid in food crops. The polypeptides may be used to design and/or identify inhibitors of those enzymes that may be used to design and/or identify inhibitors of those enzymes that may be used to design and/or increase class and as markers for the genetic and physical mapping of the genes and as markers for traits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 ThrileileTyrGlyLeuileGluArgAlaLysPheProSerAspSerHisThrTyrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspSerGlyAsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGlnGluAsp
                                                                                                                                                                                                                                                                                                        New tyrosine biosynthetic enzyme, chorismate dismutase, proteins and nucleic acids, useful for facilitating design and/or identifying inhibitors of those enzymes that may be used as herbicides and for producing antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1223 BP; 341 A; 284 C; 312 G; 286 T; 0 U; 0 Other;
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                                                                       99US-00454279
                                                                                                          98US-0110845P
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                                                                                                                                              FALCO S C.
FAMODU O O.
LEE J.
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P-PSDB; ABU08092.
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Best Local Similarity:
US2002184658-A1
                                                                       03-DEC-1999;
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                                   05-DEC-2002
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(LEEJ/)
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261

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Hamilton CM; Allen K, Mulpuri

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The present sequence is that of a full-length cDNA encoding Arabidopsis thaliana chorismate mutase-3 (CM), an enzyme that catalyses the conversion of chorismate to prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine biosynthesis. CM is essential for plant growth; inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense (see ABA91401) and sense polynucleotides, double-stranded RNA and ribozymes, and related expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that produce seedless fruit. CM is also a target for the identification of herbicides, and methods are provided for using CM in the identification of herbicide candidates. Methods are also provided for identification of herbicide candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development
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Sequence 1217 BP; 349 A; 273 C; 235 G; 360 T; 0 U; 0 Other;

	Sequence IZI/ BF; 349 A; Z/3 C; Z35 G; 350 I; U U; U Otner;	
Alignment Pred. No. Score: Percent S Best Loca Query Mat	Alignment Scores: 2.18e-67 Length: 1217 Score: 654.50 Matches: 128 Percent Similarity: 67.98\$ Conservative: 44 Best Local Similarity: 50.59\$ Mismatches: 80 Ouery Match: 6 Gaps: 1	
US-10-624	0-624-061-16 (1-261) x ABA91395 (1-1217)	
ò	ArgGluAspLeu	luAsp 29
qq	 	 AGGAC 391
٥x	luArgAlaLysPheProSerAsn	YrAsp 49
ΩP	392 AGTATTATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ATGAC 451
δy	50 GluLysTyrAlaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsn	ysAsn 69
Db .	452 GAGGATGCCTTTACTATGGAAGGGTTTCAAGGATCTTTAGTTGAGTTTATGGTCAGAGA	GAGAA 511
ò	70 ThrGlualaileGlnalaLysAlaGlyArgTyrLysAsnProGluGluAsnAlaPhePhe	hePhe 89
Db	512 ACTGAAAAGCTCACGCAAAGGTGGACAGGTACAAGAGTCCTGATGAGCATCCCTTTTTC	 TTTTC 571
ò	90 ProGluAsnLeuProProSerIleValProSerTyrSerPheLysGlnPheLeuHi	isPro 109
QQ	572 CCACAATGCTTGCCTGAACCTATCCTTCTTCTATTCAATACCCACAGGTTTTGCATGT	ATCGT 631
δ	110 GlyAlaAlaSerIleAsnIleAsnLysSerIleTrpLysMetTyrPheLysGluLeuLeu	euLeu 129
Db	632 TGCGCCGAATCGATAAACATCAACAAGAAGGTGTGGAATATGTATTTCAAACACCTTCTC	TICIC 691
ζ,	130 ProLeuleuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAspLeu	spleu 149
Ор	692 CCCAGACTGGTCAAGCCAGGGGATGACGGTAATTGTGGTTCAGCTGCTCTGTGACACA	ACACA 751
ολ	150 SerLeuLeuGlnSerIleSerArgArglleHisTyrGlyLysPheValAlaGluValLy	alLys 169
Db	752 AIGTGTTTGCAGATACTTTCAAAGAGAATTCACTTGCGTAAATTTGTTGCTGACGCCAAG	CCAAG 811
δλ	170 PheArgAspAlaProGlnAspTyrGluProLeulleArgAlaLysAspLysGluGlyLeu	lyLeu 189
QQ	812 TTTCGTGAAAATCCTGCTGCCTATGAAACAGCTATCAAAGAACAAGACCGGACACAGCTG	AGCTG 871
οy	ysLeuLeuThrPheThrSerValGluGluThrVal	ysLys 209
ДС	872 ATGCAACTTCTAACGTACGGTTGAAGAAGTAGTCAAGAAGAGAGTTGAGATCAAA	TCAAA 931
٥٨	210 AlaValValPheGlyGlnGluValAsnLeuAsnSerAspAspAsnAspAsnGluAsn	luAsn 228
q <sub>a</sub>	932 GCCAGAATTTTTGGTCAAGACATAACGATTAACGACCCAGAAACTGAAGCTGATCCTTCC	CTTCC 991

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248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of an antisense oligonucleotide that is specific for Arabidopsis thaliana chorismate-mutase-2 (CM) mRNA. CM catalyses the conversion of chorismate to prephenate in a branch of the shikimate pathway leading to phenylalanine and tyrosine bisynchesis. It is essential for plant growth, inhibition of CM gene expression in plant seedlings results in severe chlorosis, reduced growth and developmental abnormalities. The invention provides compositions for the modulation of plant growth or development using CM antisense and sense polynucleotides, double-stranded RNA and ribozymes, and related expression cassettes and vectors. The compositions are particularly useful for the modulation and inhibition of plant growth, and for generating male sterile plants or plants that produce seedless fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AspSerGlyAsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGlnGluAsp 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compounds useful for modulating and inhibiting plant growth and development, by using chorismate synthase and chorismate mutase as targets which are essential for plant growth.
229 ArglysPheAspProSerValAlaSerSerLeuTyrLysAsnTrpValIleProLeuThr
                Hamilton CM;
Allen K, Mulpuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1217 BP; 360 A; 235 C; 273 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      Arabidopsis chorismate mutase-3 antisense polynucleotide.
                                                                              1052 AAGGAAGTCCAAATTGAGTACTTGCTTAGAAGACTGGAT 1090
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                                                         LysGluValGlnValGluTyrLeuLeuArgArgLeuAsp
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Zayed A, Ascenzi RA,
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Query Match:
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90 ProGludsnieuProProSerileValProSerTyrSerPheLysGlnPheLeuHisPro 109
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                                                                                                                                                                                                                                                                                                                                            527
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286 GCCAGAATITITIGGICAAGACATAAACGACCCAGAAACIGAAGCIGATCCTICC 227
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                      130 ProLeuLeuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                     526 cccagactegrcaagccagggargacggraarreregrcagcrectcrcrerereaca 467
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                                                                      50 GluLysTyrAlaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsn 69
30 ThrileileTyrGlyLeuIleGluArgAlaLysPheProSerAsnSerHisThrTyrAsp
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Search completed: September 25, 2004, 03:07:48 Job time : 439 secs •

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US-09-454-279-15
Sequence 15, Application US/09454279
Sequence 15, Application US/09454279
Sequence 15, Application US/09454279
Sequence 15, Application US/09454279
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Lee, Jian-Ming
TILLEO TIVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BBL299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER PILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 1020
US-09-610-040-5

US-09-454-279-7

US-09-454-279-1

US-09-454-279-1

US-09-157-884-1

US-09-134-010C-1864

US-09-134-010C-1864

US-09-134-010C-1864

US-09-134-010C-1864

US-09-139-989-5

US-09-319-989-5

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US-09-319-989-8

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US-09-107-532A-1190

US-09-107-532A-1183

US-09-107-532A-183

US-09-107-532A-183

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US-09-107-532A-183

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US-09-107-532B-11

US-09-112-580-1

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Mismatches:
Indels:
Gaps:
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CRGANISM: Glycine max
US-09-454-279-15
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-MODEL=frame+ p2n.model -DEV=xlh
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2_1/USFTO_SPOO1/US10624061/runat_24092004_092407_16935/app_query.fasta_1.455
-Q=/Cgn2_1/USFTO_SPOO1/US10624061/runat_B1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=ECt -THR MAX=100 -THR MIND=0 -ALIGN=15
-MODEL-CAL -OUTFMT=pto -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624061_@CGN 1_1 69 @runat_24092004_092407_16935 -NOFU=6 -ICPU=3
-NOMAP -LARGEQUERY 'NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV INMEOUT=120 -WARN TIMEOUT=20 -THREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FCAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 13, Appli
Sequence 11, Appli
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Sequence 7, Appli
                                                                                                                                                                        September 25, 2004, 02:59:07; Search time 90 Seconds (without alignments) 1609.359 Million cell updates/sec
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                                                                                                                                                                                                                                                                 US-10-624-061-16
1339
1 MAKAAEQSPDSGNVYTLASV......NWVIPLTKEVQVEYLLRRLD 261
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Sequence 6,
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/cgn2_6/ptddata/2/ina/5A_COMB.seq:*
/cgn2_6/ptddata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                              nucleic search, using frame_plus_p2n model
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US-09-610-040-3
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US-09-610-040-8
US-09-454-279-13
US-09-610-040-4
US-09-610-040-10
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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243
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                                                                                                                                                                                                                          ---AsnValTyrThrLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                        59 CysGlySerLeuValGluPheValValLysAsnThrGluAlaIleGlnAlaLysAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ArgTyrLysAsnProGluGluAsnAlaPhePheProGluAsnLeuProProSerIleVal
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162
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Matches:
Conservative:
Mismatches:
Indels:
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                             TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
SEQ ID NO 3
LENGTH: 1006
                                                                                    Alignment Scores:
Pred. No.:
                                                        US-09-610-040-3
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APPLICANT: Davis, Keith
APPLICANT: Davis, Keith
APPLICANT: Davis, Keith
APPLICANT: Davis, Carch
APPLICANT: Homilton, Carch
APPLICANT: Hamilton, Carch
APPLICANT: Hoffman, Neil
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS
TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
FILE REFERENCE: 9128-14
CURRENT APPLICATION NUMBER: US/09/610,040
CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NGS: 11
SOFTWARE: Patentin version 3.0
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  ArgGluAspLeuValArgGlnGluAspThrIleIleTyrGlyLeuIleGluArgAlaLys
                  83 AGAGAGTITIGGITAGGCAAGAGAGATACCATCATITATGGICTCATTGAGAGAGCCAAG
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US-09-610-040-3
Sequence 3, Application US/09610040
Patent No. 6465217
GENERAL INFORMATION:
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US-00-454-279-5
| Sequence 5, Application US/09454279
| Sequence 5, Application US/09454279
| Patent No. 6627798
| GABREAL INFORMATION:
| APPLICANT: Fanco, S. Carl
| APPLICANT: Eamodu, Omolayo O. | APPLICANT: Eamodu, Omolayo O. | APPLICANT: Lee, Jian-Ming ITILE OF INVENTION: APPLICATION NUMBER: US/09/454,279
| CURRENT FILING DATE: 1999-12-03 | EARLIER APPLICATION NUMBER: US/09/454,279 | CURRENT FILING DATE: 1999-12-04 | UNMBER OF SEQ ID NOS: 22 | SOFTWARE: Microsoft Office 97 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | IBNGTH: 525 | 
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ORGANISM: Glycine max
PEATURE:
NAME/KEX: unsure
LOCATION: (432)
PEATURE:
NAME/KEY: unsure
LOCATION: (514)
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NAME/KEY: unsure

LOCATION: (516)

US-09-454-279-5
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APPLICANT: Boyes, Keith
APPLICANT: Boyes, Couglas
APPLICANT: Moesener, Jeffrey
APPLICANT: Gorlach, John
APPLICANT: Gorlach, John
APPLICANT: Hoffman, Neil
APPLICANT: Adelas
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS
TITLE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
CURRENT APPLICANTON NUMBER: US/09/610,040
CURRENT APPLICATION NUMBER: US/09/610,040
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                                   Sequence 9, Application US/09610040 Patent No. 6465217 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-610-040-9
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Db 196 TCATTGGTGGAATTTGTTAAGAATACAGAGGCCATTCAAGCTAAGGCTGGAAGATAC 255  81 LysAsnProGludluAsnAlaPhePheProGluAsnLeuProProSerIleValProSer 100  256 AAAAACCTGAAGAAAACGCCTTCTTCCCAGAAATTTACCACCATCAATTGTGCCATCT 315  Qy 101 TyrSerPheLysGlnPheLeuHisProGlyAlaAlaSerIleAsnIleAsnLysSerIle 120	RESULT 5 US-040-2 Sequence 2, Application US/09610040 Sequence 2, Application US/09610040 Sequence 2, Application US/09610040 Sequence 2, Application US/09610040 Sequence 2, Application September 1 INFORMATION: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 Applicant: September 2 September 3	** 50.38* Instances: 7  51.98* Indels: 8  4 A Gaps: 1  1) x US-09-610-040-2 (1-1207)  1) yasnvaltyrthrLeuAlaServalArgGluAs  STGAGAGTTTGACTCTTGAAGCTATTAGAAACTC

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                                                          Percent Similarity:
Best Local Similarity:
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                             Alignment Scores
   ; ORGANISM: OF
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                                                                         AspSerGlyAsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGlnGluAsp
                                       GATGAGAGTGAGAGTTTGACTCTTGAAGGTATTAGAAACTCTTTGATCCGTCAAGAGGAC
                                                            ThrilelleTyrGlyLeulleGluArgAlaLysPheProSerAsnSerHisThrTyrAsp
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; Sequence 13, Application US/09454279
; Patent No. 6627798
; GENERAL INFORMATION:
; APPLICANT: Fance, S. Carl
; APPLICANT: Fancedu, Omclayo O.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: ARCAMIC AMINO ACID BIOSYNTHETIC ENZYMES
; TITLE OF INVENTEDBY US NA
; CURRENT APPLICATION NUMBER: US/09/454,279
; CURRENT FILING DATE: 1999-12-03
; EARLIER APPLICATION NUMBER: 60/110,845
; BARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
LENGTH: 1231
 US-10~624-061-16 (1-261) x US-09-610-040-8 (1-1207)
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TATGGATCCAGTGCTCTTTGTGACACGATCTGCTTGCAGGCGCTCTCCAAAAGAATTCAC
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                            Conservative:
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Indels:
                                                                                                  US-10-624-061-16 (1-261) x US-09-454-279-13 (1-1231)
    Length:
Matches:
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                                                                                                                            Sequence 4, Application US/09610040 Patent No. 6465217 GENERAL INFORMATION:
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US-09-610-040-4
                                                                                                                                                                                             Woesner, Jeffrey
Gorlach, Jorn
Hamilton, Carol
Hoffman, Neil
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|CAAGATTGGTGAAAGAAGGAAGTGATGGTAATGCTGGATCCAGTGCTCTTTGTGACACA 656
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GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famedu, omolayo O.
APPLICANT: Famedu, omolayo O.
APPLICANT: Famedu, omolayo O.
APPLICANT: Famedu, omolayo O.
APPLICANT: Pamedu, omolayo O.
APPLICANT: Pamedu, omolayo O.
APPLICANT: Balsoy US NA
ITULE OF INVENTION: ARONGATIC AMINO ACID BIOSYNTHETIC ENZYMES
ITULE REFERENCE: Balsoy US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER PILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: MICROSOFT Office 97
SEQ ID NO 11
LENGTH: 1223
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Matches:
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70.36%
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Best Local Similarity:
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CRGANISM: Zea mays
US-09-454-279-11
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APPLICANT: Hamilton, Carol
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Ascenzi, Robert
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHASE
FILE OF INVENTION: CHORISMATE MUTASE EXPRESSION OR ACTIVITY IN PLANTS
FILE REFERENCE: 9128.14
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CURRENT FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 4
LENGTH: 1217
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PheArgAspAlaProGlnAspTyrGluProLeulleArgAlaLysAspLysGluGlyLeu 189
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                         90 ProGluAsnLeuProProSerlleValProSerTyrSerPheLysGlnPheLeuHisPro
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APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Ended, Omolayo O.
APPLICANT: Lee, dian-Ming
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
TILE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE MICROSOFT Office 97
SEQ ID NO 17
LENGTH: 780
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Best Local Similarity:
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TITLE OF INVENITON: METHODS AND COMPOSITIONS FOR THE MODULATION OF CHORISMATE SYNTHAS
TITLE OF INVENITON: METHODS AND COMPOSITIONS FOR ACTIVITY IN PLANTS
TITLE OF INVENITON: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHOR: MUTHO
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           SerLeuleuGlnSerIleSerArgArgileHisTyrGlyLysPhevalAlaGluValLys 169
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; Sequence 10, Application US/09610040
; Patent No. 6465217
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APPLICANT: Davis, Keith
APPLICANT: Woessner, Jeffrey
APPLICANT: Gorlach, Jorn
APPLICANT: Hamilton, Carol
APPLICANT: Hoffman, Neil
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Zayed, Adel
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	::::         AGATCTTCCACCACCT	aAlaSerIleAsnIle	CITITECITACATAGGICIGIGIGAAIGAIGCAATAI BIDTOLBILBIATASAGIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ATTCACTGCGGATGGC	uLeuGlnSerIleSer)          TCTGCAGGCTCTCTCA	gAspAlaProGlnAsp' :[          AGACGCGCTCAAGAT	SLeuleuThrPheThr	CTTACTAACGTTCACG	sAlaValValPheGlyGlnGluValAsnL	GATATTTGGACAGAAT	AsnGluAsnArgLysPheAspProSerV	TGACAGTCACTGTAAA	eProLeuThrLysGluv :                GCCTTTAACGAAGGATC										COMPOSITIONS FOR THE	THSE EAFKESSION C	510,040				
 GAGTTCTTCGTTCGGGAAGCCGAGGTCC GluGluAsnAlaPhePheProGluAsnL	::: .GATGTTCCATTCTTCTCTCZ	LysGlnPheLeuHisProGlyAlaAlaSerIleAsnIleAsnLysSerIleT	ccasagginigenting Tyrphelysginlenlengrole	TTCAATGAATTGCTACCATT	AlaAlaAsnAspLeuSerLe      GTTGCATTAGATTTTGCATG	PheValAlaGluValLysPheArgAspAlaProGlnAspTyrGluProLeuI :::                 TATGTTGCTGAGGTGAATTCAAAAAGGCCCCTCAAGATTATAGCCCAACAA	AspLysGluGlyLeuMetLy	 GACACTAATGCTCTGATGAA	LysArgValGluLysLysAlaVa	AGAGTAGAGAAGAAGCCAAG	AsnSerAspAspAsnAspAsnGluAsnArgLysPheAspProSerV	AAGCAAGATGGTGATGCCTG	beulyrbysasnirbvalll          CTATATGATATGTGGGTAAT	ArgArgLeuAsp 261	610 CGGCGTCTTGAC 621		Squence 6, Application US/09610040	rion: ss. Douglas	Davis, Keith Woessner Jeffrey	Gorlach, Jorn Hamilton Carol	Hoffman, Neil Kloti Andreas	Zayed, Adel Ascenzi Robert	TITLE OF INVENTION: METHODS AND COMPOSITION TITLE OF INVENTION: CHOPTEMBAR MITTARE BY	: 9128.14	ATION NUMBER: US/09/3 DATE: 2000-07-05 DAG: 11	to wersion 3.0		ORGANISM: Arabidopsis thaliana 9-610-040-6	
 	Db 70 GAA	Oy 104 Lys(	124	190	Qy 144 Thri Db 250 ACAC	Qy 164 Pheter 164 Pheter 164 Db 310 TATC	Oy 184 Lys	Db 370 AAG	204	430	220		238 Seri	Oy 258 Arg?	Db 610 CGGC	RESULT 12	Sequence 6, Appl Patent No. 64652	GENERAL INFORMATION: APPLICANT: Boves. D	APPLICANT: Davis, Keith			APPLICANT: Zay	TITLE OF INVENT	FILE REFERENCE:	CURRENT FILING DATE:	SOFTWARE: Paten : SEO ID NO 6	; LENGTH: 5176 ; TYPE: DNA	S-0	

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3 GAGTICTICGITCGGGAAGCCGAGGICCTGCACGCCAAGGCTGGACACTAICAAAAGCCA
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Patent No. 6627798
GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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         ----AsplysGluGlyLeuMetLysLeuLeuThrPheThrS 197
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                                                                                                            alAsnLeuAsnSerAspAspAspAsnGluAsnArg----------
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APPLICANT: Falco, S. Carl
APPLICANT: Fancol, Omolayo O.
The Applicant Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Emedu, Omolayo O.
APPLICANT: Les o'Jan-Ming
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
TITLE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER PILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 22
                                                                                                                                                                                                                                 4609 AAGAGGTTCAAGTGGAGTACTTGCTCAGAAGACTGGAC 4646
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Patent No. 6627798
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| LOCATION: (551)
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| NAME/KEY: unsure
| LOCATION: (565)
| FEATURE:
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84 GluGluAsnAlaPhePheProGluAsnLeuProProSerIleValProSerTyrSerPhe
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                                               63 GAAGATGTTCCATTCTCTCTCAGATCTTCCACCACCTGTTTCCTACCAAAGGTCGC
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APPLICANT: Falco, S. Carl
APPLICANT: Fancdu, Omolayo O.
APPLICANT: Lee, Jian-Ming
TITLE OF INVEXTION: ARONATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 60/110,845
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFWARE: Microsoft Office 97
SEQ ID NO
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21 ArgGluAspLeuValArgGlnGluAspThrileileTyrGlyLeuIleGluArgAlaLys 40
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Percent Similarity:
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LOCATION: (547)
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             (526)
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Sequence 972, Appl
Sequence 77, Appl
Sequence 5, Appli
Sequence 737, Appl
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Publication No. US20020184658A1
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Fandu, Omclayo O.
TITLE OF INVENTION: ARONATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REFERENCE: BE1299 US NA
CURRENT APPLICATION NUMBER: US/09/454,279
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: G0/110,845
SAFLIGE FILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
ILENGTH: 1020

LENGTH: 1020

TYPE: DNA
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               ALIGNMENTS
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-WODEL-frame+_p2n.model -DEV=x1h
-Q=CGGIZ_1VGPTO_SPOO1/USJO64361/runat_24092004_092409_17014/app_query.fasta_1.455
-Q=CGGIZ_1VGPTO_SPOO1/USJO64461/runat_24092004_092409_17014/app_query.fasta_1.455
-Q=DB=biblished_Applications_NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOOLLGN=200 -TRA SCORE=pct -THR MAX=100
-TRAMS=human40.cdi -LIST=45 -DOOLLGN=200 -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=USI0624061_@CGN 1 1 537 @runat_24092004_092409_17014
-NGPUS = .TCPUS 3 -NO MMAP -LARGEQUERY -NGS_GCRES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOPP=10 -XGAPEXT=0.5
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2571.891 Million cell updates/sec
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| cgn2_6/ptodata1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO6_NEW PUB.seq:*
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| cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
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| cgn2_6/ptodata1/pubpna/USO9_NEW PUB.seq:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                   nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES FILE REFERENCE: BB1299 US NA CURRENT APPLICATION NUMBER: US/10/624,061
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US/09/454,279
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,845
PRIOR PILING DATE: BARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 1020
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ORGANISM: Glycine max
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Rovalio, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7639
LENGTH: 1079.
110 ATGGCCAAAGCAGCAGAACAAAGTCCTGATTCTGGGAATGTGTACACGCTAGCTTCTGTG 169
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                                                                                                                                                                                                                                                             Sequence 7639, Application US/10425114, Publication No. US20040034888A1, GENERAL INFORMATION:
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ORGANISM: Glycine max
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US-10-425-114-7639
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APPLICANT: La Rosa Thomas J
APPLICANT: Anount State Control of K
APPLICANT: ANOUNT LAND Without Short Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 93036
LENGTH: 1653
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                                                                                                                                                                                                 650 ATTCGAGCTAAGGATAAGAATGGATTGATGATTGTTGACATTTACAAGCGTTGAAGAG
                                                                                                         181 IleArgAlaLysAspLysGluGlyLeuMetLysLeuLeuThrPheThrSerValGluGlu
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                                                                                                                                                                                                                                                                                                                                                              221 SerAspAspAspAsnGluAspArgLysPheAspProSerValAlaSerSerLeuTyr
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US-10-424-599-93036
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Mon Sep 27 07:44:36 2004

Query Match: 72.44% Indels: 0 DB: 13 Gaps: 0	-10-624-061-16 (1-261) x US-10-425-114-15059 (1-992)	Vy 63 ValgiubheVallyaAshThrGlualaileGinAlaiysAlaGlyArgTyriysAssn 82 	Oy 83 ProGluGluAsnAlaPhePheProGluAsnLeuProProSerIleValProSerTyrSer 102	Oy . 103 PhelysGlnPheLeuHisProGlyAlaAlaSerIleAsnLysSerIleTrpLys 122	123 MetTyrPheLysG          :::  182 ATGTATTTCCAAG	Oy 143 GInThralaAlaAsnAspLeuSerLeuGlnSerIleSerArgArgIleHisTyrGly 162	302 AAGTITGTAGGTGAAATTCAGGGATGCTCCTCAAGACTACGAGCCTTTAATTCGA	183 AlaLyshspLysGluGlyLeuMetLysLeuLerThrPheThrSerValGluGluThrVal 2	Qy 203 ArglysArgValGluLysLysAlaValValPheGlyGluGluValAsnLeuAsnSerAsp 222	Oy 223 AsphandspanGluasnarglysPheAspProSerValalaSerSerLeuTyrLysAsn 242	243 TrpValIleP	TE, TEANSGENIC
	QY         81 LysAsnProGluGluAsnAlaPhePheProGluAsnLeuProProSerIleValProSer         100	101 TyrSerPheLysGlnPheLeuHisProGlyalaAlaSer1leAsn1leAsnLysSerlle	DD 747 IACTCCTTCAAACAGTTTTTGCATCCTGGAGCTTCAATTAACATTAACAGTCCATC 806 QY 121 TrpLysMetTyrPheLysGluLeuLeuProLeuLeuAlaThrSerGlyAspAspGlyAsn 140	807		181 987		221 SerAspAspAsnAspAsnAspAsnAspAspAssAspAssAspAssAspAssAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAsnAspAspAsnAspAspAsnAspAspAsnAspAspAspAspAspAspAspAspAspAspAspAspAspA	241	Db 1167 AAAAATTGGGTGATACCCCTTACCAAGGAGGTTCAGGTTGAGTACCTATTGCGGCGTCTA 1226 Qy 261 Asp 261	Db 1227 GAC 1229	RESULT 5  US-10-425-114-15059  US-10-425-114-15059  Sequence 15059, Application US/10425114  PUBLication No. US20040034888A1  PUBLication No. US20040034888A1  PUBLICANT: Liu, Jingdong  APPLICANT: Liu, Jingdong  APPLICANT: Screen,

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Length:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                              ATTCACTACGGTAAATTTGTAGCTGAGGTCAAATTCAGAGATGCTCCACAAGATTACGAG 540
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601 gaagaatggttaagaagagagtgcagaagaaaggagaaacgtttggacaagaagaaaa 660
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                                                                                              1 MetalaLysAlaAlaGluGlnSerProAspSerGly-----AsnValTyrThrLeuAla
                                                                                                                                       19 SerValArgGluAspLeuValArgGlnGluAspThrileIleTyrGlyLeuIleGluArg
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                     Conservative:
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                                                                         US-10-624-061-16 (1-261) x US-09-938-842A-972 (1-798)
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Matches:
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIPL300-3
CURRENT PEPLICATION NUMBER: US (99/938, 842A
CURRENT FILING DATE: 2001-08-24
PRICR APPLICATION NUMBER: US 60/227, 866
PRICR PILING DATE: 2000-08-24
PRICR FILING DATE: 2000-06-24
PRICR FILING DATE: 2000-06-22
PRICR FILING DATE: 2000-06-22
PRICR FILING DATE: 2000-06-22
PRICR FILING DATE: 2000-06-22
PRICR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 972
LENGTH: 788
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APPLICANT: Davis, Couglas,
APPLICANT: Davis, Keith
APPLICANT: Hamilton, Carol
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Motes
APPLICANT: Mossner, Jeffrey
APPLICANT: Zayed, Adel
APPLICANT: Ascenzi, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: MODULATION OF CHORISMATE SYNTHASE AND CHORISMATE MUTASE
TITLE OF INVENTION: MODULATION OR ACTIVITY IN PLANTS
FILE REPERENCE: 2035DIVI
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 09/610,040
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 11
SOUTHARE FASESEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-267-763-9
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Best Local Similarity:
Query Match:
DB:
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US-10-267-763-9/c
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SEQ ID NO 9
LENGTH: 1006
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Pred. No.:
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APPLICANT: Dayis, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Abdreas
APPLICANT: Abdreas
APPLICANT: Zayed, Adel
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS POR THE
TITLE OF INVENTION: MODULATION OF CHORLSMATE SYNTHASE
TITLE OF INVENTION: EXPRESSION OR ACTIVITY IN PLANTS
TITLE OF INVENTION: 2003-10.
CURRENT APPLICATION NUMBER: US/10/267,763
CURRENT FILING DATE: 2000-10-09
FRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetAlaLysAlaAlaGluGlnSerProAspSerGly-----AsnValTyrThrLeuAla 18
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LeuAsnSerAspAsnAspAsnGluAsnArgiysPhe----AspProSerValAla
                                                         SerSerLeuTyrLysAsnTrpVallleProLeuThrLysGluValGlnValGluTyrLeu
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-267-763-3
Sequence 3, Application US/10267763
Publication No. US20030077687A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
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Davis, Keith
Hamilton, Carol
Hoffman, Neil
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ORGANISM: Arabidopsis
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Best Local Similarity:
Query Match:
DB:
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SOFTWARE: Microsoft Office 97; SEQ ID NO 5; LENGTH: S25; TYPE: DNA ORGANISM: Glycine max FRANURE: NAME/KEY: unsure; LOCATION: (432); FEATURE: LOCATION: (514); FEATURE: LOCATION: (514); FEATURE: LOCATION: (514); FEATURE: LOCATION: (514); LOCATION: (514); FEATURE: LOCATION: (514); LOCATION: (516)
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                               MetalaLysAlaAlaGluGlnSerProAspSerGly-----AsnValTyrThrLeuAla 18
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US-09-454-279-5

Sequence 5, Application US/09454279

Sequence 7, Application No. US20020184658A1

GENERAL INFORMATION:

APPLICANT: Panco, S. Carl

APPLICANT: Pencodu, Omolayo O.

APPLICANT: Lee, Jian-Ming

TITLE OF INVENTION: AROWATIC AMINO ACID BIOSYNTHETIC ENZYMES

FILE REPERENCE: BB1299 US MS.

CURRENT APPLICATION NUMBER: US/09/454,279

CURRENT FILING DATE: 1999-12-03

EARLIER APPLICATION NUMBER: 60/110,845

NUMBER OF SEQ ID NOS: 22
             US-10-624-061-16 (1-261) x US-10-267-763-9 (1-1006)
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                                                                                                       MetAlaLysAlaAlaGluGlnSerProAspSerGlyAsnValTyrThrLeuAlaSerVal
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US-10-624-061-5
Sequence 5, Application US/10624061
Publication No. US20040019929A1
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, Man-Ning
TITLE OF INVENTION: AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES
FILE REPRENCE: BB1299 US NA
CURRENT APPLICATION NUMBER: US/10/624,061
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        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                   US-10-624-061-16 (1-261) x US-09-454-279-5 (1-525)
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                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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Conservative:
Mismatches:
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             APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Mang, Xun
ITILE OF INVENTION: STRESS-REGULATED GENES OF PLA:
ITILE OF INVENTION: SAME, AND METHODS OF USE
ITILE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/224,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 737
LENGTH: 1005
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Matches:
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68.08%
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CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US/09/454,279
PRIOR FILING DATE: 1999-12-03
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 60/110,845
PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE Microsoft Office 97
LENGTH: 525
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Matches:
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Best Local Similarity:
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NAME/KEY: unsure
LOCATION: (432)
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NAME/KEY: unsure
LOCATION: (514)
FEATURE:
NAME/KEY: unsure
LOCATION: (516)
FEATURE:
LOCATION: (516)
US-10-624-061-5
                                                                                                                        TYPE: DNA
ORGANISM: Glycine
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US-09-938-842A-737
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; Sequence 737, Application US/09938842A; Patent No. US20020160378A1; GENERAL INFORMATION:

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PLANTS, TRANSGENIC PLANTS CONTAINING
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Sequence 2, Application US/10267763

Sequence 2, Application US/10267763

Sequence 2, Application US/10267763

Sequence 2, Application No. US20030077687A1

SPELICANT: Boyes, Douglas

APPLICANT: Boyes, Douglas

APPLICANT: Hamilton, Carol

APPLICANT: Hoffman, Nail

APPLICANT: Accenzi, Robert

APPLICANT: Accenzi, Robert

APPLICANT: Accenzi, Robert

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

TITLE OF INVENTION: METHODS AND CHORISMATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OR ACTIVITY IN PLANTS

TITLE OF INVENTION: EXPRESSION OR ACTIVITY IN PLANTS

TITLE OF INVENTION: SYPRESSION OR ACTIVITY IN PLANTS

TITLE OF INVENTION: SYPRESSION OR ACTIVITY IN PLANTS

TITLE OF INVENTION NUMBER: US/10/267,763

CURRENT APPLICATION NUMBER: US/200-00-09

PRIOR FILING DATE: 2000-07-05

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO S. 11

LENGTH: 1207
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190 MetLysLeuLeuThrPheThrSerValGluGluThrValArgLysArgValGluLysLys
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ORGANISM: Arabidopsis
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Best Local Similarity:
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Pred. No.:
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Sequence 737, Application US/09938842A

Publication No. US20040009476A9

Publication No. US20040009476A9

Publication No. US20040009476A9

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Areps, Joel

APPLICANT: Areps, Joel

APPLICANT: Sth, Tong

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE OF INVENTION: SAME, AND METHODS OF USE

FILE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 1005

TYPE: DNA

TYPE: DNA

TYPE: DNA

TYPE: DNA

TYPE: DNA
                                                                                                                    GlyalaAlaSerIleAsnIleAsnLysSerIleTrpLysMetTyrPheLysGluLeuLeu 129
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      ||||||| ::: ||||||| ||||||| ||||||| ACTGAGAAGCTTCACCTTTCTTC 462
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                                                        ---LysPheAspProSerValAlaSerSerLeuTyrLys 241
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Command line parameters:
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-O-CH2_1/USFO_spool/US10624661/runat_selected_1-DOPCL=0_-LOOPEXT=0
-UNINS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNINS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-DBV_TIMBOUT=120 -WARN TIMBOUT=30 -TRIREADS=1 -XGAPOP=10 -XGAPDXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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## SUMMARIES

Score   Match Length DB   ID   Description	Sul	91	Query	Lengt	B	QI	escription
1         917         68.5         56.3         10         AW766427         AW66427         AW666427           2         895         66.8         64.8         10         AW775942         BA734625         BA775942         BA775942         BA775942         BA775942         BA775942         BA775942         BA775174         BA775942         BA775942         BA775942         BA775942         BA775942         BA775942         BA775942         BA775944          BA7759444         BA7759444	! ! ካሪሠፋኒንው!	166		1			
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27         590.5         44.1         557         14         CB829043         CB829043           28         586.5         43.8         516         14         CB827444         CB827444           29         586.5         43.8         516         14         CR827444         AAG12424           30         580         43.3         865         13         BU693059         CF480460           31         579.5         43.3         761         14         CF480460         CF480460           32         579         43.2         501         14         CB826052         CF4810460           34         573.5         42.8         501         14         CB826052         CF481060           35         573.5         42.8         549         14         CB82614         CB82614           36         572.5         42.8         549         14         CB82614         CB82614           37         57.5         42.8         549         14         CB82614         CB82614           37         57.5         42.8         549         14         CB82614         CB826666           38         571.5         42.7         529         14	26	. 06		53	-	844	28445 LjNEST
28         586.5         43.8         516         14         CB827444         CB827444         CB827444           29         583.5         43.6         680         9         AJ612241         BU652242           31         579.5         43.3         63.9         14         CF840460         CF460460           32         579.5         43.2         63.9         10         ER660542         ER660542           34         573.5         43.2         63.0         14         CF840460         CF840460           35         573.5         42.8         63.0         14         CF843707         CF8206052           35         573.5         42.8         63.9         10         ER660542         CF843707           36         572.5         42.8         63.9         14         CF843707         CF826664           37         42.8         63.9         14         CB82614         CB826676           39         571.5         42.7         68.0         13         CR000410         CR000410           39         57.1         42.6         68.0         14         CF862676         CR481222           40         56.4         42.1         72	27	90	٠,	55		904	29043 LJNEST
29         583.5         43.6         680         9         AJG12241         AJG12241           30         580         43.3         881         13         BR663059         BUG93059           31         579.5         43.3         61         14         CR823059         CF449305           32         578.5         43.2         639         10         BE660542         CF84306           34         573.5         42.8         639         10         BE67076         CF443707         CF84306           35         572.5         42.8         639         10         BE577489         CF84366           36         572.5         42.8         549         14         CR828614         CR828614         CR8286614           37         571.5         42.9         14         CR828614         CR8286614         CR8286614           37         57.1         42.6         680         13         CR828614         CR8286614         CR8286614           38         57.1         42.6         54.9         14         CR828614         CR8286614         CR8286614           39         567.5         42.8         54.1         14         CR828614         CR828614	89	86	· ~	21	-	744	27444 LjNEST
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36 572.5 42.8 549 14 CB828614 CB828614 CB828614 37 571.5 42.7 529 14 CB828676 CA82676 CB82676 38 571.5 42.7 529 14 CB828676 CA82676 CA	35	Ŋ	ď.	59	Н	7748	77489 L48-2335
37 571.5 42.7 529 14 CB226768 CB26768 CB26768 CB26768 38 571 42.6 680 13 CA080410 CA080410 CB29238 40 567.5 42.1 14 CB329238 CF481222 CF48122 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 CF4812 C	36	72	ď	54	Н	861	28614 LINESTRE
38 571 42.6 680 13 CA080410 CA080410 39 567.5 42.4 541 14 CB829238 CB829238 41 564 42.1 725 14 CF486896 CF486896 42 561 41.9 696 14 CD919148 CD919148 43 559 41.7 595 10 BE445201 BE445201 CB622596 44 552.5 41.1 10 BF430733 BF430733	37	71	ď.	52	Н	3676	26768 LJNEST66
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40     564     42.1     683     14     CF481822     CF48122       41     563.5     42.1     725     14     CF486896     CF486896       42     561     41.9     696     14     CD919148     CD918189       43     551     41.7     595     10     BB445201     BE445201       44     552.5     41.7     390     14     CB622596     CB622596       45     550.5     41.1     71     10     BF430733     BF430733	39	67	ď.	54	1	2923	29238 LJNEST95
41 563.5 42.1 725 14 CF486896 CF486899 42 561 41.9 696 14 CD919148 CD919146 43 559 41.7 595 10 BE445201 BE4452591 44 552.5 41.3 800 14 CB622596 CB622590 45 550.5 41.1 10 BF430733 BF430733	40	2	αi.	39	٦	3122	31222
42 561 41.9 696 14 CD919148 CD919148 43 559 41.7 595 10 BE445201 BE445201 44 552.5 41.3 800 14 CB622596 CB623596 45 550.5 41.1 10 BF430733 BF430733	•	63	ď.	72		3689	36896 POLT 40
43 559 41.7 595 10 BE445201 BE445201 BE445201 44 552.5 41.3 830 14 CB622596 CB625596 45 550.5 41.1 10 BF430733 BF430733	•	Š	ä	9	Н	1914	19148 G608,112
44 552.5 41.3 830 14 CB622596 CB622596 45 550.5 41.1 711 10 BF430733 BF430733	43		ä	Š	-	1520	45201 WHE1133
45 550.5 41.1 711 10 BF430733 BF430733	•	52	ä	60	-	2259	22596 OSIIEa09
	•	20	Ä	71	Н	3073	30733 OG04A12T

## STUBMINE TA

AW666427 563 bp mRNA linear EST 03-DEC-2001	1 sk36d12.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-4272 5' similar to SW:CHMU_ARATH P42738 CHORISMATE MUTASE	PRECURSOR ;, mRNA sequence.	AW666427	AW666427.1 GI:7478842	BST.	Glycine max (soybean)		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
RESULT 1 AW666427 LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	

84

124

365

07:44:37 2004

TITLE JOURNAL COMMENT

FEATURES

REFERENCE

Alignment Scores:

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Xhoi; The maxA was isolated from roots of dlycine max
'Supernod' plants generously donated by Dr. Gary Stacey.
The seedlings were innoculated with Bradyrhizobium
aponicus, strain USDAIIO priot to harvest. Stratagene's
CDNA synthesis Kit (catalog number 200401) was used to
synthesize the CDNA. First-strand synthesis was performed
with S-methyl dCTP, hence the ligated CDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (Va-A,C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAACAGACTCGAG(7)18V] to anchor
the primer at the S' end of the poly(A) tract. After
second-strand synthesis, the CDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The Xhoi site within the
first-strand synthesis primer was then restricted by
digestion with Xhoi; all Xhoi sites in the CDNA
constructs were size-fractionated status. The CDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' CDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript II XR Predigested with ECONI
(pBluescript II SK(+) that has been digested with ECONI
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
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Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R. eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

AW774625 648 bp mRNA linear EST 07-SEP-2000 EST333776 KV3 Medicago truncatula cDNA clone pKV3-23M13, mRNA 425 185 104 245 305 144 164 486 GATAAAGAAGGATTGATGAAATTGGTGACATTTACAAGCGTTGAAGAGACAGTGAGGGAA 545 426 GTAGCTGAGGTGAAATTCANGGATGCTCCTCAAGACTACGAGCCTTTTATTCGAGCTAAG 485 Medicago truncatula Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, ESTs from roots of Medicago truncatula after Rhizobium inoculation Unpublished (1999) 65 165 ValAlaGluValLysPheArgAspAlaProGlnAspTyrGluProLeuIleArgAlaLys 184 185 AspLysGluGlyLeuMetLysLeuLeuThrPheThrSerValGluGluThrValArgLys 204 1 (bases 1 to 648)
vaidenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M. 45 SerHisThrTyrAspGluLysTyrAlaGlnIleGlnGlyPheCysGlySerLeuValGlu PheValValLysAsnThrGluAlaIleGlnAlaLysAlaGlyArgTyrLysAsnProGlu 126 TTTGTTGTTAAGAATACAGAGGCCATTCAAGCTAAGGCTGGAAGATACAAAAACCCTGAA 85 GluAsnAlaPhePheProGluAsnLeuProProSerIleValProSerTyrSerPheLys 186 GAAAACGCCTTCTTCCCAGAAATTTACCACCATCAATTGTGCCATCTTACTCCTTCAAA 246 CAGTITITGCATCCTGGAGCTGCTTCAATTAACATTAACAAGTCCATCTGGAAAATGTAT 125 PhelysGluLeuLeuProLeuLeuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThr 145 AlaAlaAsnAspLeuSerLeuLeuGlnSerIleSerArgArgIleHisTyrGlyLysPhe 366 GCAGCTAATGATCATTATTGCAGGCCATCTCTAGAAGGATTCACTATGGAAAGTTT 105 GlnPheLeuHisProGlyAlaAlaSerIleAsnIleAsnLysSerIleTrpLysMetTyr 306 TTCCAAGAGTTACTTCCATTGGTTGCTACTTCGGGGGATGATGGAGGAAACTATGCACAAAACT Department of Plant Biology University of Minnesota 220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA TIGR sequence name: MTEBC79TK
More information is available at.
More information is available at.
More information continuedu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Locatton/Qualifiers
1. .648 Medicago truncatula (barrel medic) Email: kvandenb@cbs.umn.edu Texas A&M EST name:T258044e 205 ArgvalGluLysLysAla 210 546 GAGGTTGAAAAGAAGGCC 563 Contact: VandenBosch K GI:7718542 Tel: 612 624 2755 Fax: 612 625 1738 AW774625.1 sequence. 65 ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION TITLE JOURNAL COMMENT AUTHORS REFERENCE RESULT 2 AW774625 음 & g & QQ à 장. 염 ò 9 Dp à 셤  $\delta$ g à 8

FEATURES

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Xho1; The cDNA library was constructed From floral
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University, Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
Xho1 restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by Xho1 digestion. The
CDNA fragments were directionally cloned into the
EcoRI-Xho1 restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Back, C., Wylie, T., Underwood, K., Steptco, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Watterscon, R. and Wilson, T., Jackson, Y., Cardenas, M.,
McCann, R., Watterscon, R. and Wilson, R.
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, NO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wateson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 397.
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TR:Q9S7H4 Q9S7H4 CHORISMATE MUTASE
                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnGluAspThrIleIleTyrGlyLeuIleGluArgAlaLysPheProSerAsnSerHis
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Matches:
Conservative:
Mismatches:
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                                     saci9f08.yl Gm-c1051 Glycine max v
ID: Gm-c1051-2943 5' similar to Ti
bG36746 sequence.
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                                                                                                                                                              BG363365.1 GI:13252454
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876.00
99.41%
99.41%
                                                                                                                                                                                                          Glycine max (soybean)
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                                                                                                                                                                                                                                   Glycine max
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Best Local Similarity:
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BG363365
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Pred. No.:
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                                                                     DEFINITION
                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
  RESULT 3
BG363365
LOCUS
                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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Xhof; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Giagnock III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCATTICTAAAAAAGAGTTCATTATGGAAAGTTTGTAGCTGAAGTGAAATTCAGGGAATCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 ThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeuSerLeuLeuGln 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerIleSerArgArgIleHisTyrGlyLysPheValAlaGluValLysPheArgAspAla 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caaarcccresiririsisescrearissrrisarristrarcaccaracreasarsir 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 ProProSerIleValProSerTyrSerPheLysGlnPheLeuHisProGlyAlaAlaSer 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleAsnileAsnLysSerileTrpLysMetTyrPheLysGluLeuLeuProLeuLeuAla 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 gerrecegreargardacaacrardedaaacrecaecraecakeretereardardarrecae 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProGlnAspTyrGluProLeuIleArgAlaLysAspLysGluGlyLeuMetLysLeuLeu 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAlaLysAlaGlyArgTyrLysAsnProGluGluAsnAlaPhePheProGluAsnLeu 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCAAGACTATGAGCCTTTAATTCGGTCTAAGGACAAAGAAGGGTTGATGATGTTG
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Conservative:
Mismatches:
Indels:
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NF091B12FL 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AATGAATATACTCTTGATACAGTGAGGGAGACTTTGGTTAGACAAGAAGATACAATTGTT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGluGluAspThrlleIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 TIATCATIGLACTIGLACCATTTACCCTTCACAAAGTTTTTGCATCCTGGAGCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 GTTGCTTCCGGTGATGATGCCAACTATGCACAAACTGCAGCTAGCGACCTCTCATTGTTG
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                                                                                                                                              CAAGAGGATACCATCATTTATGGTCTCATTGAGAGAGGCCAAGTTCCCTAGCAATTCTCAC
                                                                                                                          ValLysAsnThrGluAlaIleGlnAlaLysAlaGlyArgTyrLysAsnProGluGluAsn
                                                                                                                                                                                            AlaPhePheProGluAsnLeuProProSerIleValProSerTyrSerPheLysGlnPhe
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                                                                               1 (bases 1 to 654)
Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTS from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                                    363 GAGTTACTTCCATTGCTTGCTACTTCGGGTGATGATGGCAACTATGCGCAAACTGCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Deborah A. Samac
Contact: Deborah A. Samac
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 1243
Pax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: debbys@puccini.crl.umn.edu
Minnesota sequence name:M259175e
TIGR sequence name:MTFAJ28TK
More information is available at..
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
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Medicago truncatula
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)

Contact: Dixon RA Plant Biology Division
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dev_stage="Call suspensions were subcultured every 14
days. Calls were induced six days after subculture"
/clone_lip="Elicited call culture"
/note="Vector: Lambda Zap; Calls were induced with yeast
call wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                               365 GAATCTCCTCAAGACTATGAGCCTTTAATTCGGTCTAAGGACAAAGAAGGGTTGATGAAA 424
                                                                                                                LeuGlnSerIleSerArgArgIleHisTyrGlyLysPheValAlaGluValLysPheArg 171
                                                                                                                                                     172 AspAlaProGinAspTyrGluProLeuIleArgAlaLysAspLysGluGlyLeuMetLys 191
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                                                                                                                                                                                                                                                                                                                                                                      192 LeuLeuThrPheThrSerValGluGluThrValArgLysArgValGluLysLysAlaVal
132 LeuAlaThrSerGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeuSerLeu
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/mol type="mRNA"
/do_xef="wexnois"80"
/clone="NF09181218"
/tissue_type="Developing flowers"
/dev_stage="Developing flowers"
/dev_stage="Developing, flowers"
/dev_stage="Developing, flowers"
/dev_stage="Developing, flowers and flowers in early transition into pods."
/clone="Nector: Lambda Zap; cDNA was prepared from polyA+
/note="Vector: Lambda Zap; cDNA was prepared from polyA+
/note="Nector: Lambda Zap; cDNA was prepared from polyA+
/note="Nector: Lambda Zap; cDNA was prepared flowers and flowers transitioning into pods. The cDNA was
/clone and packaged into the Uni Zap XR vector
/stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
using extages thelper Phage and the E. coli strain
/xil-Blue MRR' (Stratagene). Excised plasmids were plated
using SOLR cells."
                                                                                                                                                                                                                (bases 1 to 696)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
Unpublished (2001)
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580 221 7391
Fax: 580 221 7390
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 696 Std Brror: 0.00
Plate: 091 row: B column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
Location/Qualiflers
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McCann, R., Waterston, R. and Wilson, R.

In Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Undervao,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 TTATCATTGTCACTTGTTCCATCTTACCCCTTCACAAAGTTTTTGCATCCTGGAGCCGCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 TCGATTAACATAAACAAGTCCTTAAGGAAAATGTACTTTCATGACCTGCTTCCATGTTC 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AlaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsnThrGluAla 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnValTyrThrLeuAlaSerValArgGluAspLeuValArgGlnGluAspThrlleIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 GTTGCTTCCGGTGATGATGGCAACTATGCACAACTGCAGCTAGCGACCTCTCATTGTTG
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59.30%
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311

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RESULT 8 BI420527

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

101

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Jeases 1 to 477)

S Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., S Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Thaising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Materston, R. Sahir, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-53-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL97356 GM-C1019 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: GM-C1019-435 5' similar to SW:CHMU_ARATH P42738 CHORISMATE MUTASE PRECURSOR; MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glýcine max subrantae, Streptophyta; Embryophyta; Tracheophyta; Subrayota; Viridiplantae; Streptophyta; Embryophyta; Ore eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TrplysMetTyrPheLysGluLeuLeuProLeuLeuAlaThrSerGlyAspAspGlyAsn 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 TATGCACAAACTGCAGCTAGCGATCTTTCATTATTGCAGGCAATCTCTAGAAGGATTCAT
---GAATGAATGATGTTTTCCCTGGAGTCTGTG
                                                                ArgGluAspLeuValArgGlnGluAspThrIleIleTyrGlyLeuIleGluArgAlaLys
                                                                                                                                                                                                                                     SerLeuValGluPheValValLysAsnThrGluAlaileGlnAlaLysAlaGlyArgTyr
                                                                                                                                                                                                                                                                                                                      LysAsnProGluGluAsnAlaPhePheProGluAsnLeuProProSerIleValProSer
                                                                                                                                                                                                                                                                                                                                                                                                        TyrSerPhelysGlnPheleuHisProGlyAlaAlaSerIleAsnIleAsnLysSerIle
                                                                                                                                                   41 Phe ProSerAsnSerHisThrTyrAspGluLysTyrAlaGlnIleGlnGlyPheCysGly
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LjNEST58b9r Lotus japonicus nodule library 5 and 7 week-old Lotus
corniculatus var. japonicus CDNA 5', mRNA sequence.
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Streptrophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                                        TyrSerPheLysGlnPheLeuHisProGlyAlaAlaSerIleAsnIJeAsnLysSerIle
                                                     372 TACTCCTTCAAACAGTTTTTGCATCCTGGAGCTGCTTCAATTAACATTAACAAGTCCATC
                                                                                             TrpLysMetTyrPhelysGluLeuLeuProLeuLeuAlaThrSerGlyAspAspGlyAsn
                                                                                                                          432 TGGAAAAT-TATTTCCAAGAGTTACTTTCATTGGTTGCTACTTCGGGGGATGAATGGAAC
                                                                                                                                                                                                                                                                  160 sTyrGlyLysPheValAlaGluValLysPheArgAspAlaProGlnAspTyrGluProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lotus corniculatus var. japonicus"
/mol_type="mRNA"
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
/db_xrege="5 and 7 week-old plants"
/clone_lib="Lotus japonicus nodule library 5 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 605)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Udvardi MK
Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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Query Match:

No.:

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                                                                                                                                                                                                   /lab host="DH10B (Gibco BRL)"
/clone_lib="Gm-c1019"
/clone_lib="Gm-c1019"
/clone_lib="Gm-c1019"
/note=="Vector: pSPORTI (life Technologies); Site_1: Not I;
Site_2: Sal I: This cDNA library was constructed_from mRNA
isolated from immature seed coats (200-300 mgs) of
greenhouse grown plants. The library was prepared using
the Life Technologies Superscript cDNA library
construction kit. Complementary DNA was synthesized from
mRNA using a poly (dT) sequence with a Not I restriction
site. Sal I linker adapters were ligated to the
blunt-ended cDNA fragments followed by Not I digestion.
The cDNA fragments were directionally cloned into the Not
I-Sal I restriction site of the pSPORTI vector. The
ligated cDNA fragments were transformed into E.coli
ElectroMax BH10B host cells (Gibco BRL). This library was
constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .41 TyralaGlnThralaAlaAsnAspLeuSerIeuLeuGlnSerIleSerArgArglleHis 160
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                                                                                                             /mol_type="mRNA"
/db xrefe="taxon:3847"
/clone="genome systems cLone ID: Gm-c1019-435"
/tissue_type="immature seed coats of greenhouse grown
plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrGlyLysPheValAlaGluValLysPheArgAspAlaProGlnAspTyrGluProLeu
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Matches:
Conservative:
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Insert Length: 653 Std Error: 0.00 Seg primer: -40RP from Gibco High quality sequence stop: 447.
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BG239446 abbond Library Type Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1032-2453 5' similar to TR:Q9S7H4 Q9S7H4 CHORISMATE MUTASE; mRNA sequence.
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Shoemaker, R., Kaim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Balla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                   65 CAAGCTATGGCTGGAAGGTACCAAAACCCTGAAGAAATGCCTTCTTCCCAGAACATTTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleasnileAsniysSerileTrpLysMetTyrPheLysGluLeuLeuProLeuLeuAla 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 ThrserGlyAspAspGlyAsnTyrAlaGlnThrAlaAlaAsnAspLeuSerLeuLeuGln 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 GCGTCCGGTGATGATGGCAACTATGCACAACTGCAGCTAGCGATCTTTCATTATTGCAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerileSerArgArgileHisTyrGlyLysPheValAlaGluValLysPheArgAspAla 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 CCTCAAGACTATGAGCCTTTAATTCGTGCTAAGGACACAGAAGGTTGATGAAATTATTG
                                                                                                                                                                                                                                                                                                       SAAATCCCGGGTTTTTGTGGCTCATTGGTCGAATGTGTTCAAAACACTGAGGCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ProproSerIleValProSerTyrSerPheLysGlnPheLeuHisProGlyAlaAlaSer
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Glycine max
Eukaryota; Viridiplant
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82.35%
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LjNEST70f7r Lotus japonicus nodule library 5 and 7 week-old Lotus consiculatus var. japonicus cDNA 5', mRNA sequence.
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
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Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                   TrpLysMetTyrPhelysGluLeuProLeuLeuAlaThrSerGlyAspAspGlyAsn
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                                                                                                           SerAspAspAsnAspAsnGluAsnArgLysPheAspProSerValAlaSerSerLeuTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="mRNA"
/cultivar="Gifu (B-129)"
/cultivar="Gifu (B-129)"
/de xef="kaxon:347 week-old plants"
/dev_targe="5 and 7 week-old plants"
/clone_lib="Lotus japonicus nodule library 5 and 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tobases 1 to 529)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional Unpublished (2000)
Contact: Udvardi MK
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Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: udvardi@mpimp-golm.mpg.de
Seq primer: T7
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Location/Qualifiers
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/organism="Sorghum bicolor"
//organism="Sorghum bicolor"
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//olliva="Bar623"
//db xref="taxcn:4558"
//db xref="taxcn:4558"
//db host="Bh130 H03 A002"
//lab host="Bh103-T] phage-resistant E. coli"
//loone lib="Salicylic acid-treated seedlings"
//ore="Vector: pME18S-F13; Site 1: Xho1; Site 2: Xho1; The library was prepared from poly44 RNA from seedlings"
//nore="Vector: pME18S-F13; Site 1: Xho1; Site 2: Xho1; The library was prepared from poly44 RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 1 mM salicylic acid (SA). Roots and shock were harvested affer 2 T and 72 hr and material from both time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into different brail sites is CACCATGTG, 3-prime Draili site is CACCATGTG, 3-prime Draili site is CACCATGTG; 3-prime Draili site is
   SAI_30_H03.gl_A002 Salicylic acid-treated seedlings Sorghum bicolor CDA77426.1 GI:31333689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Taxas A & M University, sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude exclude polyA.
                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panticoideae; Andropogonaee; Sorghum.

1 (Soasea 1 to 810)

Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.K., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R., Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P., Olaseinde,O., Eastman,A. and Pratt,L.H.

An EST darabase from Sorghum: salicylic acid-treated seedlings Other ESTS: Sal 30 H03.bl A002

Contact: Cordonnier-Pratt,MM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
Fax: 706 583 0210
Email: mmpratt@uga.edu
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Sorghum bicolor
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                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Eax: 314 286 1810
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800) 533 4363 or contact via email: ccu@resgen.com
High quality sequence stop: 402.
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Fax: 314 286 1810
Email: esGwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4533 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shoemaker,R., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Back,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,T., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
Public, Soybean, EST Project
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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     71
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       52 TyralaGlnIleGlnGlyPheCysGlySerLeuValGluPheValValLysAsnThrGlu
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Public Soybean EST Project
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4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
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                     372 GCCCTCAACGCAAAGGCTGGACATTATCAAAAGCCAGAAGATGTTCCATTCTTCCCTCAA
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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.igr.org; or NCBI, www.ncbi.nlm.nih.gov. when the source of the maize cDNA sequences is either Virginia Malbot, Stanford or Pat Schnable, lowa State, then clones may be requested from ZmDB:
                                                                                                                     HTC 16-0CT-2002
                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Hainey,C.P., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanaley,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
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